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68 248.2 94.0 10850 12 U02455 Cloning vec
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70 248.2 94.0 11265 6 BD094805
71 248.2 94.0 16958 6 AX665480
72 248.2 94.0 37808 6 AX001082
73 247.2 93.6 633 14 ALRPROLTS
74 244.8 92.7 565 6 AR202606
75 244.8 92.7 565 6 BD005483
76 244.8 92.7 565 14 U41728
77 244.8 92.7 874 14 RSU41727
78 244.8 92.7 10427 12 AF484679
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80 241.6 91.5 532 14 RSU41726
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98 224 84.8 3277 6 A30505
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ALIGNMENTS

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RESULT 1
AX175190 AX175:90 648 bp DNA linear PAT 03-JUL-2001
LOCUS Sequence 1 from Patent WO0142444.
DEFINITION
ACCESSION AX175:90
VERSION AX175:90.1 GI:14598581
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
        artificial sequences.
REFERENCE
1 Rivera, V., Zoltick, P. and Wilson, J. M.
AUTHORS Methods for expression of genes in primates
TITLE Patent: WO 0142444-A 1 14-JUN-2001;
JOURNAL ARIAD GENE THERAPEUTICS, INC. (US) ; THE UNIVERSITY OF PENNSYLVANIA
(US)
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QY 1 AATGAGTCTTATGCAATACCTTGTAGTCTTGCACATGTTAAACGATGAGTTAGCAACA 60
Db 349 AATGAGTCTTATGCAATACCTTGTAGTCTTGCACATGTTAAACGATGAGTTAGCAACA 408
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGTAGTGGTAGGTCAGCA 120

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Db 409 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGTAGTGGTAGGTCAGCA 468
QY 121 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGAGTGGAGCAACCACTAAATT 180
Db 469 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGAGTGGAGCAACCACTAAATT 528
QY 181 CGCATTTGCAGAGATATTGTTATTTAAAGTGGCTAGCTCGATACATAAAGCCATTGGACC 240
Db 529 CGCATTTGCAGAGATATTGTTATTTAAAGTGGCTAGCTCGATACATAAAGCCATTGGACC 588
QY 241 ATTACACCACTTTGGTGTGCACCTC 264
Db 589 ATTACACCACTTTGGTGTGCACCTC 612
RESULT 2
AX175195 AX175:195 648 bp DNA linear PAT 03-JUL-2001
LOCUS Sequence 6 from Patent WO0142444.
DEFINITION
ACCESSION AX175:195
VERSION AX175:195.1 GI:14598586
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
        artificial sequences.
REFERENCE
1 Rivera, V., Zoltick, P. and Wilson, J. M.
AUTHORS Methods for expression of genes in primates
TITLE Patent: WO 0142444-A 6 14-JUN-2001;
JOURNAL ARIAD GENE THERAPEUTICS, INC. (US) ; THE UNIVERSITY OF PENNSYLVANIA
(US)
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ORIGIN

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Query Match 100.0%; Score 264; DB 6; Length 648;
Best Local Similarity 100.0%; Pred. No. 1.2e-65;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGAGTCTTATGCAATACCTTGTAGTCTTGCACATGTTAAACGATGAGTTAGCAACA 60
Db 349 AATGAGTCTTATGCAATACCTTGTAGTCTTGCACATGTTAAACGATGAGTTAGCAACA 408
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGTAGTGGTAGGTCAGCA 120
Db 409 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGTAGTGGTAGGTCAGCA 468
QY 121 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGAGTGGAGCAACCACTAAATT 180
Db 469 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGAGTGGAGCAACCACTAAATT 528
QY 181 CGCATTTGCAGAGATATTGTTATTTAAAGTGGCTAGCTCGATACATAAAGCCATTGGACC 240
Db 529 CGCATTTGCAGAGATATTGTTATTTAAAGTGGCTAGCTCGATACATAAAGCCATTGGACC 588
QY 241 ATTACACCACTTTGGTGTGCACCTC 264
Db 589 ATTACACCACTTTGGTGTGCACCTC 612
RESULT 3
AX743955 AX743:955 7086 bp DNA linear PAT 14-MAY-2003
LOCUS Sequence 3 from Patent WO03031630.
DEFINITION
ACCESSION AX743:955
VERSION AX743:955.1 GI:30722652
KEYWORDS
SOURCE synthetic construct

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ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Pazio,V., Rinaldi,M., Sorzogni,L., Tonon,G. and Orsini,G.
TITLE Multi-cistronic vectors for gene transfer protocols
JOURNAL Patent: WO 0301630-A 3 17-APR-2003;
Keryos Spa (IT)
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/db_xref="taxon:32630"

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Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 60
DB AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 1737
QY 61 TGCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTCGTAAGTAAGTGGTACGA 120
DB TGCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTCGTAAGTAAGTGGTACGA 1736
QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
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QY 181 CCGCATTCGACAGATATTGTATTAGTCCCTAGCTGCATACATAAAGCCATTGACC 240
DB CCGCATTCGACAGATATTGTATTAGTCCCTAGCTGCATACATAAAGCCATTGACC 1557
QY 241 ATTCACCAATTTGGTGTGCACCTC 264
DB ATTCACCAATTTGGTGTGCACCTC 1533

RESULT 4
BD268239 8238 bp DNA linear PAT 17-JUL-2003
LOCUS Adenovirus vector, packaging cell line, composition and method for
production and use.
DEFINITION
ACCESSION BD268239
VERSION BD268239.1 GI:33078007
KEYWORDS JP 2002534130-A/43.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 8238)
AUTHORS Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and
Skripchenko,Y.
TITLE Adenovirus vector, packaging cell line, composition and method for
production and use.
JOURNAL Patent: JP 2002534130-A 43 15-OCT-2002;
NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
COMMENT OS Artificial Sequence
PN JP 2002534130-A/43
PD 15-OCT-2002
PF 14-JAN-2000 JP 2000593765
PR 14-JAN-1999 US 60/115920
PI GLEN ROBERT NEMEROW,DANIEL J VON SEGGERN,PAUL L HALLENBECK, PI
SUGAN C STEVENSON,YELENA SKRIPCHENKO
PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00,
PC C12N5/10,
PC C12N7/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC
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Best Local Similarity 99.6%; Pred. No. 2.5e-65;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 60
DB AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 600
QY 61 TGCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTCGTAAGTAAGTGGTACGA 120
DB TGCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTCGTAAGTAAGTGGTACGA 660
QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
DB TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 720
QY 181 CCGCATTCGACAGATATTGTATTAGTCCCTAGCTGCATACATAAAGCCATTGACC 240
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QY 241 ATTCACCAATTTGGTGTGCACCTC 264
DB ATTCACCAATTTGGTGTGCACCTC 804

RESULT 5
ALRSV40LTR 330 bp DNA linear VPL 30-NOV-1999
LOCUS Rous sarcoma virus-SV40 recombinant long terminal repeat DNA.
DEFINITION
ACCESSION M27329
VERSION M27329.1 GI:341667
KEYWORDS LTR; long terminal repeat.
SOURCE Simian virus 40
ORGANISM Simian virus 40
REFERENCE 1 (bases 1 to 330)
AUTHORS Weber,F. and Schaffner,W.
TITLE Enhancer activity correlates with the oncogenic potential of avian
retroviruses
JOURNAL EMBO J. 4 (4), 949-956 (1985)
MEDLINE 85257513
PUBMED 2990916
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source Location/Qualifiers
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virus; Unknown which part is from which virus."

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Best Local Similarity 99.6%; Pred. No. 7.5e-65;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGGCAATGCTAAACGATGAGTTAGCAACA 60
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QY 61 TGCCTTACAGGAGAGAGAAAGACCGTGCATGCCGATTCGTAAGTAAGTGGTACGA 120
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QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
DB 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
QY 181 CCGCATTCGACAGATATTGTATTAGTCCCTAGCTGCATACATAAAGCCATTGACC 240

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Db 181 CGCATTGACAGAGATTGTTATTAAAGTGCCTAGCTGCTGATACATAAAGCCATTGACC 240
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Qy 241 ATTCACCAATTTGGTGCACCT 263
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Db 241 ATTCACCAATTTGGTGCACCT 263
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RESULT 6
ALRDCJ 700 bp DNA linear VRL 11-MAR-1994
LOCUS Rous sarcoma virus (Schmidt-Ruppin A) circle junction.
ACCESSION L29390 J02018 N00022
VERSION L29390.1 GI:459678
KEYWORDS circle junction; long terminal repeat (LTR); terminal repeat.
SOURCE Rous sarcoma virus
ORGANISM Rous sarcoma virus
REFERENCE 1 (sites)
DEFINITION Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
AUTHORS Swanstrom,R., DeLorbe,W.J., Bishop,J.M. and Varmus,H.E.
TITLE Nucleotide sequence of cloned unintegrated avian sarcoma virus DNA:
viral DNA contains direct and inverted repeats similar to those in
transposable elements
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (1), 124-128 (1981)
MEDLINE 81223697
PUBMED 6264426
REFERENCE 2 (sites)
AUTHORS Mirra,T.K., Grandgenett,D.P. and Parsons,J.T.
TITLE Avian retrovirus pp32 DNA-binding protein. I. Recognition of
specific sequences on retrovirus DNA terminal repeats
JOURNAL J. Virol. 44 (1), 330-343 (1982)
MEDLINE 83059884
PUBMED 6292495
REFERENCE 3 (bases 1 to 700)
AUTHORS Maroney,A.C., Qureshi,S.A., Foster,D.A. and Brugge,J.S.
TITLE Cloning and characterization of a thermolabile v-src gene for use
in reversible transformation of mammalian cells
ONCOGENE 7 (6), 1207-1214 (1992)
JOURNAL 92278773
MEDLINE 1375718
PUBMED
COMMENT Original source text: Rous sarcoma virus (Schmidt-Ruppin strain,
subgroup A) Unintegrated circularized DNA.
Bases 1-700 from Proc. Natl. Acad. Sci. U.S.A. 78. 124-128 (1981)
Bases 21-680 from J. Virol. 44, 330-343 (1982)
For linear genome see separate entries.
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Best Local Similarity 99.6%; Pred. No. 6.8e-65;
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Qy 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTGTAACGATGAGTTAGCAACA 60
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Qy 181 CGGCATTGACAGATATTGTTATTTAAGTGCCTAGCTGCTGATACATAAAGCCATTGACC 240
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Query Match 99.0%; Score 261.4; DB 14; Length 700;
Best Local Similarity 99.6%; Pred. No. 6.8e-65;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTGTAACGATGAGTTAGCAACA 60
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Qy 181 CGGCATTGACAGATATTGTTATTTAAGTGCCTAGCTGCTGATACATAAAGCCATTGACC 240
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Db 201 CGGCATTGACAGATATTGTTATTTAAGTGCCTAGCTGCTGATACATAAAGCCATTGACC 260
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Query Match 99.0%; Score 261.4; DB 14; Length 700;
Best Local Similarity 99.6%; Pred. No. 6.8e-65;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTGTAACGATGAGTTAGCAACA 60
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Db 21 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTGTAACGATGAGTTAGCAACA 80
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Qy 241 ATTCACCAATTTGGTGCACCT 263
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RESULT 7
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DEFINITION environment).
ACCESSION V01168 N00022
VERSION V01168.1 GI:61497
KEYWORDS Avian sarcoma virus
SOURCE Avian sarcoma virus
ORGANISM Avian sarcoma virus
REFERENCE 1 (bases 1 to 700)
DEFINITION Viruses; Retrovirdae; Retroviridae; Avian type C retroviruses.
AUTHORS Swanstrom,R., DeLorbe,W.J., Bishop,J.M. and Varmus,H.E.
TITLE Nucleotide sequence of cloned unintegrated avian sarcoma virus DNA:
viral DNA contains direct and inverted repeats similar to those in
transposable elements
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (1), 124-128 (1981)
MEDLINE 81223697
PUBMED 6264426
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Best Local Similarity 99.6%; Pred. No. 6.8e-65;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTGTAACGATGAGTTAGCAACA 60
|||||
Db 21 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGCTGTAACGATGAGTTAGCAACA 80
|||||
Qy 61 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATCCGATGCTGGAAGTAAGTGGTTACGA 120
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Db 81 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATCCGATGCTGGAAGTAAGTGGTTACGA 140
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Qy 121 TCGTGCCCTATTAGGAGGACGACGCGGTCTGACATGGATTGACGACCACTAAATTT 180
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Db 141 TCGTGCCCTATTAGGAGGACGACGCGGTCTGACATGGATTGACGACCACTAAATTT 200
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Qy 181 CGGCATTGACAGATATTGTTATTTAAGTGCCTAGCTGCTGATACATAAAGCCATTGACC 240
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Db 201 CGGCATTGACAGATATTGTTATTTAAGTGCCTAGCTGCTGATACATAAAGCCATTGACC 260
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Qy 241 ATTCACCAATTTGGTGCACCT 263
|||||
Db 261 ATTCACCAATTTGGTGCACCT 283
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RESULT 8
ALRDAI 1239 bp DNA linear VRL 12-APR-1999
LOCUS Rous sarcoma virus (Schmidt-Ruppin A), 5' LTR and gag gene.
DEFINITION
ACCESSION L29198 J02018 J02026 J02338 N00020

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VERSION L29198.1 GI:459671
 KEYWORDS gag protein; long terminal repeat (LTR); polyprotein.
 SEGMENT 1 of 2
 SOURCE Rous sarcoma virus
 ORGANISM Rous sarcoma virus
 REFERENCE 1 (sites)
 AUTHORS Viruses; Retroviral viruses; Retroviridae; Alpharetrovirus.
 TITLE Nucleotide sequence of cloned unintegrated avian sarcoma virus DNA: viral DNA contains direct and inverted repeats similar to those in transposable elements
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (1), 124-128 (1981)
 MEDLINE 81223697
 PUBMED 6264426
 REFERENCE 2 (sites)
 AUTHORS Swanson, R., Varmus, H.E. and Bishop, J.M.
 TITLE Nucleotide sequence of the 5' noncoding region and part of the gag gene of Rous sarcoma virus
 JOURNAL J. Virol. 41 (2), 535-541 (1982)
 MEDLINE 82192582
 PUBMED 6281455
 REFERENCE 3 (sites)
 AUTHORS Misra, T.K., Grandgenett, D.P. and Parsons, J.T.
 TITLE Avian retrovirus pp32 DNA-binding protein. I. Recognition of specific sequences on retrovirus DNA terminal repeats
 JOURNAL J. Virol. 44 (1), 330-343 (1982)
 MEDLINE 83059884
 PUBMED 6292495
 REFERENCE 4 (sites)
 AUTHORS Petersen, R.B., Hensel, C.H. and Hackett, P.B.
 TITLE Identification of a ribosome-binding site for a leader peptide encoded by Rous sarcoma virus RNA
 JOURNAL J. Virol. 51 (3), 722-729 (1984)
 MEDLINE 84292449
 PUBMED 6088795
 REFERENCE 5 (sites)
 AUTHORS Hughes, S., Mellstrom, K., Kosik, E., Tamanoi, F. and Brugge, J.
 TITLE Mutation of a termination codon affects src initiation in reversible transformation of mammalian cells
 JOURNAL Mol. Cell. Biol. 4 (9), 1738-1746 (1984)
 MEDLINE 85016324
 PUBMED 6092936
 REFERENCE 6 (sites)
 AUTHORS Maroney, A.C., Qureshi, S.A., Foster, D.A. and Brugge, J.S.
 TITLE Cloning and characterization of a thermostable v-src gene for use in reversible transformation of mammalian cells
 JOURNAL Oncogene 7 (6), 1207-1214 (1992)
 MEDLINE 92278773
 PUBMED 1375718
 COMMENT The following base pairs can be found in the references listed below:
 1-350 J. Virol. 44, 330-343 (1982)
 230-1239 J. Virol. 41, 535-541 (1982)
 1-330 Proc. Natl. Acad. Sci. U.S.A. 78, 124-128 (1981) 230-619 Mol. Cell. Biol. 4, 1738-1746 (1984)
 253-318 J. Virol. 51, 722-729 (1984)
 For a description of the life cycle and the RNA transcripts of Rous sarcoma virus, see the Rous sarcoma virus Prague C strain entry. Positions 331-348 are complementary to the 3' stem of host-encoded Trp-tRNA. Trp-tRNA binds to virion RNA at this site and serves as a primer for DNA synthesis by reverse transcription. The gag-Pr76, gag-pol-Pr180, and env-Pr95 reading frames all begin with the fourth 'atg' start codon of their respective mRNAs at position 601-603. [4] used anisomycin to stall ribosomes at the initiation codon and found that ribosomes were stalled at the initiation codon at position 270-272 indicating that this 'atg' start codon is actually used to produce a 7 amino acid leader peptide. [4] found a small peptide that comigrated with a synthetic 7 amino acid peptide identical to the peptide predicted from the sequence following this start codon.
 The src cds is the only coding region that does not utilize the 'atg' start codon at position 601-603. In the src mRNA this start codon is followed by an in-frame stop codon. [5] mutated this 'tga' stop codon to 'cga' and found that an src protein extended at

the N-terminal end was produced. [5] predicts that the 'atg' start codon at position 601-603 is utilized in the 21S src mRNA to produce a 9 amino acid leader peptide. Cells infected with the mutant RSV encoding the extended src-p63 exhibit a different morphology than those infected with wild-type RSV producing src-p60.
 The Prague strain subgroup C Rous sarcoma virus has been shown to encode a transcriptional activator protein from a reading frame that corresponds to positions 601-618 (exon 1) and 902- greater than 1239 (partial exon 2), (see Prague C entry).

FEATURES

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 GRVSPPECIETKATERRIDKGEVETTVQORDAKWAPPEATPKVTGTCYHCCTGA
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 Best Local Similarity 99.8%; Pred. No. 6.3e-65;
 Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGAGTCTTATGCAATACTCTTGTAGTCTTGCACATGTAAGTGTAGCA 60
 Db 1 AATGAGTCTTATGCAATACTCTTGTAGTCTTGCACATGTAAGTGTAGCA 60
 QY 61 TGCCTTACAGGAGAGAAACGACCGTCAGTCGATGGTGAAGTGTAGCA 120
 Db 61 TGCCTTACAGGAGAGAAACGACCGTCAGTCGATGGTGAAGTGTAGCA 120
 QY 121 TGTGTCCTTATTAGGAAGCAACAGACGGGCTGTGACATGGATTGGACCACTAAATT 180
 Db 121 TGTGTCCTTATTAGGAAGCAACAGACGGGCTGTGACATGGATTGGACCACTAAATT 180
 QY 181 CGGCAATTCAGAGATATTGTATTTTAAGTCCTAGCTGCATACATATAAGCCATTGACC 240
 Db 181 CGGCAATTCAGAGATATTGTATTTTAAGTCCTAGCTGCATACATATAAGCCATTGACC 240
 QY 241 ATTACACCATTTGGTGTGCACT 263
 Db 241 ATTACACCATTTGGTGTGCACT 263

RESULT 9

ALRDA2

LOCUS ALRDA2 3256 bp DNA linear VRL 12-APR-1999
 DEFINITION Rous sarcoma virus (Schmidt-Ruppin A) env-src-3'LTR.
 ACCESSION L29199 J02038 J02026 J02352 K01194 K01195 N00021
 VERSION L29199.1 GI:459672
 KEYWORDS c-myc proto-oncogene; kinase; protein kinase; src oncogene.
 SEGMENT 2 of 2
 SOURCE Rous sarcoma virus
 ORGANISM Rous sarcoma virus
 REFERENCE 1 (sites)
 AUTHORS Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
 TITLE Cernilofsky,A.P., DeLorbe,W., Swanson,R., Varmus,H.E., Bishop,J.M.,
 TITLE The nucleotide sequence of an untranslated but conserved domain at
 the 3' end of the avian sarcoma virus genome
 JOURNAL Nucleic Acids Res. 8 (13), 2967-2984 (1980)
 MEDLINE 81053726
 PUBMED 81053726
 REFERENCE 2 (sites)
 AUTHORS Cernilofsky,A.P., Levinson,A.D., Varmus,H.E., Bishop,J.M.,
 TITLE Nucleotide sequence of an avian sarcoma virus oncogene (src) and
 proposed amino acid sequence for gene product
 JOURNAL Nature 287 (5779), 198-203 (1980)
 MEDLINE 81052295
 PUBMED 8253794
 REFERENCE 3 (sites)
 AUTHORS Swanson,R., DeLorbe,W.J., Bishop,J.M. and Varmus,H.E.
 TITLE Nucleotide sequence of cloned unintegrated avian sarcoma virus DNA:
 viral DNA contains direct and inverted repeats similar to those in
 transposable elements
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (1), 124-128 (1981)
 MEDLINE 81223697
 PUBMED 6264426
 REFERENCE 4 (sites)
 AUTHORS Swanson,R., Varmus,H.E. and Bishop,J.M.
 TITLE Nucleotide sequence of the 5' noncoding region and part of the gag
 gene of Rous sarcoma virus
 JOURNAL J. Virol. 41 (2), 535-541 (1982)
 MEDLINE 82192582
 PUBMED 6281465
 REFERENCE 5 (sites)
 AUTHORS Hughes,S.H.
 TITLE Sequence of the long terminal repeat and adjacent segments of the
 endogenous avian virus Rous-associated virus 0
 JOURNAL J. Virol. 43 (1), 191-200 (1982)
 MEDLINE 82269131
 PUBMED 6286997
 REFERENCE 6 (sites)
 AUTHORS Misra,T.K., Grandgenett,D.P. and Parsons,J.T.
 TITLE Avian retrovirus pp32 DNA-binding protein. I. Recognition of
 specific sequences on retrovirus DNA terminal repeats
 JOURNAL J. Virol. 44 (1), 330-343 (1982)
 MEDLINE 83059884
 PUBMED 6292495
 REFERENCE 7 (sites)
 AUTHORS Cernilofsky,A.P., Levinson,A.D., Varmus,H.E., Bishop,J.M.,
 TITLE Corrections to the nucleotide sequence of the src gene of Rous
 sarcoma virus
 JOURNAL Nature 301 (5902), 736-738 (1983)
 MEDLINE 83141780
 PUBMED 6298633
 REFERENCE 8 (sites)
 AUTHORS Sorge,J., Ricci,W. and Hughes,S.H.
 TITLE cis-Acting RNA packaging locus in the 115-nucleotide direct repeat
 of Rous sarcoma virus
 JOURNAL J. Virol. 48 (3), 667-675 (1983)
 MEDLINE 84036404
 PUBMED 6313966
 REFERENCE 9 (sites)
 AUTHORS Hughes,S. and Kosik,E.
 TITLE Matogenesis of the region between env and src of the SR-A strain of
 Rous sarcoma virus for the purpose of constructing

helper-independent vectors
 JOURNAL Virology 136 (1), 89-99 (1984)
 MEDLINE 84251740
 PUBMED 6330999
 REFERENCE 10 (sites)
 AUTHORS Petersen,R.B., Hensel,C.H. and Hackett,P.B.
 TITLE Identification of a ribosome-binding site for a leader peptide
 encoded by Rous sarcoma virus RNA
 JOURNAL J. Virol. 51 (3), 722-729 (1984)
 MEDLINE 84292449
 PUBMED 6088795
 REFERENCE 11 (sites)
 AUTHORS Hughes,S., Mellstrom,K., Kosik,E., Tamanoi,F. and Brugge,J.
 TITLE Mutation of a termination codon affects src initiation
 JOURNAL Mol. Cell. Biol. 4 (9), 1738-1746 (1984)
 MEDLINE 85036324
 PUBMED 6092936
 REFERENCE 12 (sites)
 AUTHORS Resnick,R., Omer,C.A. and Paras,A.J.
 TITLE Involvement of retrovirus reverse transcriptase-associated RNase H
 in the initiation of strong-stop (+) DNA synthesis and the
 generation of the long terminal repeat
 JOURNAL J. Virol. 51 (3), 813-821 (1984)
 MEDLINE 84292461
 PUBMED 6206236
 REFERENCE 13 (sites)
 AUTHORS Fellman,D., Garber,E.A., Cross,F.R. and Hanafusa,H.
 TITLE Fine structural mapping of a critical NH2-terminal region of p60src
 Proc. Natl. Acad. Sci. U.S.A. 82 (6), 1623-1627 (1985)
 MEDLINE 85166183
 PUBMED 2984663
 REFERENCE 14 (sites)
 AUTHORS Maroney,A.C., Qureshi,S.A., Foster,D.A. and Brugge,J.S.
 TITLE Cloning and characterization of a thermolabile v-src gene for use
 in reversible transformation of mammalian cells
 JOURNAL Oncogene 7 (6), 1207-1214 (1992)
 MEDLINE 92278773
 PUBMED 1375718
 COMMENT The bases as they are found in the references are listed below:
 1-3107 Nature 287, 198-203 (1980)
 2907-3256 Proc. Natl. Acad. Sci. U.S.A. 78, 124-128 (1981)
 2244-3176 Nucleic Acids Res. 8, 2967-2984 (1980)
 700-908 J. Virol. 43, 191-200 (1982)
 2927-3176 J. Virol. 44, 330-343 (1982)
 1-3107 Nature 301, 736-738 (1983)
 706-900 and 2791-2830 J. Virol. 48, 667-675 (1983)
 721-1140 Mol. Cell. Biol. 4, 1738-1746 (1984)
 2912-2938 J. Virol. 51, 813-821 (1984)
 873-882 and 950-1128 Virology 136, 89-99 (1984)
 1121-1173 Proc. Natl. Acad. Sci. U.S.A. 82, 1623-1627 (1985) [1]
 revised by [7].
 [7] revises [1].
 See comment in segment 1.
 The src gene is believed to have been obtained from avian DNA when
 an ALV-like virus recombined with host DNA. Homology to the c-src
 gene of chicken begins at position 1032. A direct repeat of about
 100 bp is present near either end of exon 2 the 21S (src) mRNA.
 These repeats include positions 772-899 and 2703-2799. A
 polyadenylation signal is present at position 3149-3154. [7]
 contains a revision of the sequence in [1]. Individual revisions
 are not noted in sites.
 [9] mutated the 'tga' stop codon at position 1057-1059 to 'cga' and
 found that the mutant strain produced an src protein extended at
 the NH-terminal end.
 [10] created a synthetic Rous sarcoma virus lacking the direct
 repeat 5' of src-p60 and with Clal sites flanking src-p60 to create
 a vector capable of expressing genes inserted in place of src-p60
 (see RSV vector in synthetic section).
 [11] used mutants with alterations in the N-terminal region of the
 src-p60 gene to determine the requirements for N-myristylation of
 residue at amino acid position 2 (position 1126-1128 of this
 sequence).

Query Match	99.0%;	Score	261.4;	DB 14;	Length	3256;			
Best Local Similarity	99.6%;	Pred. No.	5.6e-65;						
Matches	262;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	AATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGGTTAACGATGAGTTAGCAACA	60						
Db	2927	AATGTAGTCTTATGCAATACTCTTGTAGTCTTGCACATGGTTAACGATGAGTTAGCAACA	2986						
QY	61	TGCCTTTACAAGGAGAGAAAACACCGCTGCATGCCGATTTGGTGGAACTTAAGSTGGTGACGA	120						
Db	2987	TGCCTTTACAAGGAGAGAAAACACCGCTGCATGCCGATTTGGTGGAACTTAAGSTGGTGACGA	3046						
QY	121	TGTTGCCCTATTAGGAGGCAACAGAGCGGCTGACATGGATTGCAAGAACCACTTAATTT	180						
Db	3047	TGTTGCCCTATTAGGAGGCAACAGAGCGGCTGACATGGATTGCAAGAACCACTTAATTT	3106						
QY	181	CGCAATGCGAGAGATTGTGATTTTAACTGSCCTAGCTCGATACAATAAACGCCATTTTGACC	240						
Db	3107	CGCAATGCGAGAGATTGTGATTTTAACTGSCCTAGCTCGATACAATAAACGCCATTTTGACC	3166						
QY	241	ATTACCAACATTTGGTGTGCACCT	263						

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7 ATTACACCAATTGGTGGCACT 3189

ABI05370      11572 bp   DNA      circular SYN 21-MAY-2003
Cloning vector RCAS-L14 DNA, complete sequence.
ABI05370
ABI05370.1   GI:28971911

Cloning vector RCAS-L14
Cloning vector RCAS-L14
artificial sequences; vectors.
1
Konaguchi,C., Kawakami,Y. and Nohno,T.
Nucleotide sequence of retroviral cloning vector, RCAS-L14
Published Only in Database (2003)
2 (bases 1 to 11572)
Location/Qualifiers
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/db_xref="taxon:224009"
1..14
/note="pBR322-derived sequence"
139..438
739..2850
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ORIGIN

Query Match 99.0%; Score 261.4; DB 12; Length 11572;
 Best Local Similarity 99.6%; Pred. No. 4.7e-65;
 Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AATGTAGCTTTATGCAATACCTCTCTGTAGTCTTGGCAACATGTAACGATGAGTACCAACA 60
 Db 139 AATGTAGCTTTATGCAATACCTCTCTGTAGTCTTGGCAACATGTAACGATGAGTACCAACA 198
 Qy 61 TGCCTTACAGGAGAGAAAAGCACCGTCATGCGAGTGGTGAAGTAAGTGGTACGA 120
 Db 199 TGCCTTACAGGAGAGAAAAGCACCGTCATGCGAGTGGTGAAGTAAGTGGTACGA 258
 Qy 121 TCGTGCCTTATTAGAGGCAACAGACGGGTCTGACATGGAATTGGAGAACCACTAAATT 180
 Db 259 TCGTGCCTTATTAGAGGCAACAGACGGGTCTGACATGGAATTGGAGAACCACTAAATT 318
 Qy 181 CGGCATTTGAGAGATTTGATTTTAACTGCTGCTGATACCAATTAAGCGCATTTGACC 240
 Db 319 CGGCATTTGAGAGATTTGATTTTAACTGCTGCTGATACCAATTAAGCGCATTTGACC 378
 Qy 241 ATTCAACCACTTGGTGCACCT 263
 Db 379 ATTCAACCACTTGGTGCACCT 401

RESULT 11
 BD261584 11627 bp DNA linear PAT 17-JUL-2003
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 DEFINITION Methods and compositions useful for modulation of angiogenesis

using tyrosine kinase Src.
 BD261584
 VERSION BD261584.1 GI:33071352
 KEYWORDS JP 2002516344-A/1.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 11627)
 AUTHORS Cheresah,D.A., Eliceiri,B. and Schwartzberg,P.I.
 TITLE Methods and compositions useful for modulation of angiogenesis
 JOURNAL using tyrosine kinase Src
 COMMENT Patent: JP 2002516344-A 1 04-JUN-2002;
 THE SCRIPPS RESEARCH INSTITUTE,THE UNITED STATES OF AMERICA
 OS Artificial Sequence
 PN JP 2002516344-A/1
 PD 04-JUN-2002
 PF 28-MAY-1999 JP 2000550976
 PR 23-MAY-1998 US 60/087220
 PI DAVID A CHERESH,BRIAN ELICEIRI,PAMELA L SCHWARTZBERG PC
 A61K38/00,A61K45/00,A61K48/00,A61P19/02,A61P29/00, PC
 A61P35/00,
 PC A61P35/02,A61P43/00,C12N9/12,C12N15/09,A61K37/02,C12N15/00 CC
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 sarcoma virus
 CC pBR322 sequences
 CC upstream
 CC upstream (numbering begins at the upstream R) CC U3
 CC R
 CC U5
 CC downstream
 CC U3
 CC U3
 CC R
 CC U5
 CC PPT
 CC splice donor (AGGT)
 CC env splice acceptor (AGGC)
 CC ClaI splice acceptor (AGGA)
 CC gag p19
 CC gag p10
 CC gag p12
 CC gag p27
 CC gag p15
 CC gag stop
 CC pol RT
 CC pol IN
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 and does not
 CC cut.
 Location/Qualifiers
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 FT misc_feature (7649)..(11258)
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 FT LTR (7166)..(7494)
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 FT misc_feature (7415)..(7494)
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 FT misc_feature (6982)..(6985)
 FT Gene (372)..(902)
 FT Gene (909)..(1094)
 FT Gene (1095)..(1814)
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Db	425	TGTTGCCCTTTATAGAAAGGCAACAGACGGGCTCAGCATGGATTGGACGACCACTAAATT	484
QY	181	COGCATTGCAGAGATATTGTATTTAAAGTGCCTAGCTGCATACATATAAACGCCATTTGACC	240
Db	485	COGCATTGCAGAGATATTGTATTTAAAGTGCCTAGCTGCATACATATAAACGCCATTTGACC	544
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Db	545	ATTCCACCATTGGTGTGCACC	566

RESULT 13

XXU42373

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

5289 bp

DN

circular SYN 05-JAN-1996

Cloning vector pOP13Cat target vector from Lacswitch System.

U42373.1

GI:1147762

Cloning vector pOP13Cat

Cloning vector pOP13Cat

artificial sequences; vectors.

1 (bases 1 to 5289)

Marsh,S.

Direct Submission

Submitted (05-DEC-1995)

Sam Marsh, Marketing, Strategene, 11011 North Torrey Pines Road, La Jolla, CA 92037, USA

Location/Qualifiers

1. 5289

/organism="Cloning vector pOP13Cat"

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source

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QY	241	ATTACACACATTGGTGTGCACC	262	
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RESULT 14					
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LOCUS	Sequence 1	from Patent	WO9942577.		
DEFINITION	AX018983	ACCESSION			
VERSION	AX018983.1	GI:10043078			
KEYWORDS	.				

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE artificial sequences.
AUTHORS Ila-Herttuala,S., Airenne,K., Kulomaa,M., Marjomaki,V. and Lehtolainen,P.
TITLE Biotin-binding receptor molecules
JOURNAL Patent: WO 9942577-A 1 26-AUG-1999;
YLA HERTTUALA SEPO (FI); AIRENNE KARI (FI); KULOMAA MARKKU (FI); MARJOMAKI VARPU (FI); LEHTOLAINEN PAULIINA (FI); EUROGENE LIMITED (GB)
FEATURES Location/Qualifiers
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CDS 1071..2273
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ORIGIN
Query Match 98.2%; Score 259.2; DB 6; Length 5177;
Best Local Similarity 98.9%; Pred. No. 2.3e-64;
Matches 261; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGGTAAACGATGAGTTAGCAACA 60
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DB 3286 CCGCATTCGACAGATATTGTTATTTAAGTCGCTAGCTCGATACATAATAAGCCATTGGACC 3345
QY 241 ATTCACACATTTGGTGTGCACCTC 264
DB 3346 ATTCACACATTTGGTGTGCACCTC 3369
RESULT 15
BD136828
LOCUS Biotin-binding receptor molecule.
DEFINITION BD136828
ACCESSION BD136828
VERSION BD136828.1 GI:23231773
KEYWORDS JP 2002504328-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 5177)
AUTHORS Herttuala,S.Y., Kulomaa,M., Lehtolainen,P., Marjomaki,V. and Airenne,K.
TITLE Biotin-binding receptor molecule
JOURNAL Patent: JP 2002504328-A 1 12-FEB-2002;
ARC THERAPEUTICS LTD
COMMENT OS Unidentified
PN JP 2002504328-A/1
PD 12-FEB-2002
PF 23-FEB-1999 JP 2000532517
PR 23-FEB-1998 GB 9803757.5,24-JUN-1998 GB 9813653.4 PI
SEPO YLA HERTTUALA, MARKKU KULOMAA, PAULIINA LEHTOLAINEN, VARPU PI
MARJOMAKI, AIRENNE
PI KARI, AIRENNE
PC C12N15/09,A61K48/00,A61P43/00,C07K14/705//A61K38/00,C12N15/00,
PC A61K37/02
CC Strandedness: Single;
CC Topology: Linear;
CC Biotin-binding receptor molecule
FH Key Location/Qualifiers
FT CDS 1071..2270.
FEATURES Location/Qualifiers
source 1..5177
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 98.2%; Score 259.2; DB 6; Length 5177;
Best Local Similarity 98.9%; Pred. No. 2.3e-64;
Matches 261; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGGTAAACGATGAGTTAGCAACA 60
DB 3106 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGGTAAACGATGAGTTAGCAACA 3165
QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCGGATTCGTCGAAAGTAAAGTGGTACGA 120
DB 3166 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCGGATTCGTCGAAAGTAAAGTGGTACGA 3225
QY 121 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
DB 3226 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 3285
QY 181 CCGCATTCGACAGATATTGTTATTTAAGTCGCTAGCTCGATACATAATAAGCCATTGGACC 240
DB 3286 CCGCATTCGACAGATATTGTTATTTAAGTCGCTAGCTCGATACATAATAAGCCATTGGACC 3345
QY 241 ATTCACACATTTGGTGTGCACCTC 264
DB 3346 ATTCACACATTTGGTGTGCACCTC 3369
RESULT 16
REASV3
LOCUS Avian sarcoma virus fragment (3' end).
DEFINITION V01167
ACCESSION V01167
VERSION V01167.1 GI:61496
KEYWORDS
SOURCE Avian sarcoma virus
ORGANISM Avian sarcoma virus
REFERENCE 1 (bases 1 to 1016)
AUTHORS Czernilofsky,A.P., DeLorbe,W., Swanstrom,R., Varmus,H.E., Bishop,J.M., Fischer,E. and Goodman,H.M.
TITLE The nucleotide sequence of an untranslated but conserved domain at the 3' end of the avian sarcoma virus genome
JOURNAL Nucleic Acids Res. 8 (13), 2967-2984 (1980)
MEDLINE 81053726
PUBMED 6253899
FEATURES Location/Qualifiers
source 1..1016
/organism="Avian sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11876"

TITLE Biotin-binding receptor molecule
JOURNAL Patent: JP 2002504328-A 1 12-FEB-2002;
ARC THERAPEUTICS LTD
COMMENT OS Unidentified
PN JP 2002504328-A/1
PD 12-FEB-2002
PF 23-FEB-1999 JP 2000532517
PR 23-FEB-1998 GB 9803757.5,24-JUN-1998 GB 9813653.4 PI
SEPO YLA HERTTUALA, MARKKU KULOMAA, PAULIINA LEHTOLAINEN, VARPU PI
MARJOMAKI, AIRENNE
PI KARI, AIRENNE
PC C12N15/09,A61K48/00,A61P43/00,C07K14/705//A61K38/00,C12N15/00,
PC A61K37/02
CC Strandedness: Single;
CC Topology: Linear;
CC Biotin-binding receptor molecule
FH Key Location/Qualifiers
FT CDS 1071..2270.
FEATURES Location/Qualifiers
source 1..5177
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Query Match 98.2%; Score 259.2; DB 6; Length 5177;
Best Local Similarity 98.9%; Pred. No. 2.3e-64;
Matches 261; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGGTAAACGATGAGTTAGCAACA 60
DB 3106 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGGTAAACGATGAGTTAGCAACA 3165
QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCGGATTCGTCGAAAGTAAAGTGGTACGA 120
DB 3166 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCGGATTCGTCGAAAGTAAAGTGGTACGA 3225
QY 121 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
DB 3226 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 3285
QY 181 CCGCATTCGACAGATATTGTTATTTAAGTCGCTAGCTCGATACATAATAAGCCATTGGACC 240
DB 3286 CCGCATTCGACAGATATTGTTATTTAAGTCGCTAGCTCGATACATAATAAGCCATTGGACC 3345
QY 241 ATTCACACATTTGGTGTGCACCTC 264
DB 3346 ATTCACACATTTGGTGTGCACCTC 3369
RESULT 16
REASV3
LOCUS Avian sarcoma virus fragment (3' end).
DEFINITION V01167
ACCESSION V01167
VERSION V01167.1 GI:61496
KEYWORDS
SOURCE Avian sarcoma virus
ORGANISM Avian sarcoma virus
REFERENCE 1 (bases 1 to 1016)
AUTHORS Czernilofsky,A.P., DeLorbe,W., Swanstrom,R., Varmus,H.E., Bishop,J.M., Fischer,E. and Goodman,H.M.
TITLE The nucleotide sequence of an untranslated but conserved domain at the 3' end of the avian sarcoma virus genome
JOURNAL Nucleic Acids Res. 8 (13), 2967-2984 (1980)
MEDLINE 81053726
PUBMED 6253899
FEATURES Location/Qualifiers
source 1..1016
/organism="Avian sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11876"

ORIGIN

Query Match 97.8%; Score 258.2; DB 14; Length 1016;
Best Local Similarity 98.9%; Pred. No. 5.5e-64;
Matches 260; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 60
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DB 687 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 746

QY 61 TGCCTTACAAGGAGAAAGACACCGTCATGCCGATGGTGGAGTAAGTGGTACGA 120
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DB 747 TACCTTACAAGGAGAAAGACACCGTCATGCCGATGGTGGAGTAAGTGGTACGA 806

QY 121 TCGTGCCTTATTAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTAAATT 180
|||||
DB 807 TCGTGCCTTATTAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTAAATT 866

QY 181 CGCATTTGAGAGATATTGTTATTTAGTGCCTAGCTGATACAAATAAGCGCCTTTGACC 240
|||||
DB 867 CGCATTTGAGAGATATTGTTATTTAGTGCCTAGCTGATACAAATAAGCGCCTTTGACC 926

QY 241 ATTCAACACATTTGGTGTGCACCT 263
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DB 927 ATTCAACACATTTGGTGTGCACCT 949

RESULT 17

AR071323
LOCUS AR071323 4965 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 1 from patent US 5910488.
ACCESSION AR071323
VERSION AR071323.1 GI:7222211
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4965)
AUTHORS Nabel, G.J., Nabel, E.G., Lew, D. and Marquet, M.
TITLE Plasmids suitable for gene therapy
JOURNAL Patent: US 5910488-A 1 08-JUN-1999;
FEATURES
source
1..4965
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 97.6%; Score 257.6; DB 6; Length 4965;
Best Local Similarity 98.5%; Pred. No. 6.6e-64;
Matches 260; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 60
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DB 260 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 319

QY 61 TGCCTTACAAGGAGAAAGACACCGTCATGCCGATGGTGGAGTAAGTGGTACGA 120
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DB 320 TGCCTTACAAGGAGAAAGACACCGTCATGCCGATGGTGGAGTAAGTGGTACGA 379

QY 121 TCGTGCCTTATTAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTAAATT 180
|||||
DB 380 TCGTGCCTTATTAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTAAATT 439

QY 181 CGCATTTGAGAGATATTGTTATTTAGTGCCTAGCTGATACAAATAAGCGCCTTTGACC 240
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DB 440 CGCATTTGAGAGATATTGTTATTTAGTGCCTAGCTGATACAAATAAGCGCCTTTGACC 499

QY 241 ATTCAACACATTTGGTGTGCACCTC 264
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DB 500 ATTCAACACATTTGGTGTGCACCTC 523

RESULT 18

Query Match 97.1%; Score 256.4; DB 6; Length 562;
Best Local Similarity 99.6%; Pred. No. 2e-63;

AX256413
LOCUS AX256413 262 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 61 from Patent WO0170816.
ACCESSION AX256413
VERSION AX256413.1 GI:16075238
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Palli, S.R., Kapitekaya, M.Z. and Cress, D.E.
TITLE Ecdysone receptor-based inducible gene expression system
JOURNAL Patent: WO 0170816-A 61 27-SEP-2001;
ROHM AND HAAS COMPANY (US)
FEATURES
Location/Qualifiers
1..262
source
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 97.4%; Score 257.2; DB 6; Length 262;
Best Local Similarity 98.9%; Pred. No. 1.3e-63;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACAT 61
|||||
DB 1 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACAT 60

QY 62 GCCTTACAAGGAGAAAGACACCGTCATGCCGATGGTGGAGTAAGTGGTACGA 121
|||||
DB 61 GCCTTACAAGGAGAAAGACACCGTCATGCCGATGGTGGAGTAAGTGGTACGA 120

QY 122 CGTGCCTTATTAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTAAATT 181
|||||
DB 121 CGTGCCTTATTAGGAGCAACAGACGGGCTCTGACATGGATTGGAGCAACCACTAAATT 180

QY 182 CGCATTTGAGAGATATTGTTATTTAGTGCCTAGCTGATACAAATAAGCGCCTTTGACC 241
|||||
DB 181 CGCATTTGAGAGATATTGTTATTTAGTGCCTAGCTGATACAAATAAGCGCCTTTGACC 240

QY 242 TTCAACACATTTGGTGTGCACCT 263
|||||
DB 241 TTCAACACATTTGGTGTGCACCT 262

RESULT 19

AX643583
LOCUS AX643583 562 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 2 from Patent WO02099100.
ACCESSION AX643583
VERSION AX643583.1 GI:28551383
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.

REFERENCE 1
AUTHORS Al-Rubeai, M. and Shuttleworth, J.
TITLE Method of production of a protein in cells which inducibly express
JOURNAL the cell cycle inhibitor protein, p21
Patent: WO 02099100-A 2 12-DEC-2002;
Lonza Biologics plc (GB)
FEATURES
Location/Qualifiers
1..562
source
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
/note="Rous Sarcoma Virus LTR promoter"

ORIGIN

Query Match 97.1%; Score 256.4; DB 6; Length 562;
Best Local Similarity 99.6%; Pred. No. 2e-63;

Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
 |||||
 Db 305 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 364
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QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
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 Db 365 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 424
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QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 180
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 Db 425 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 484
 |||||

QY 181 CGCATTTGCAGAGATTAATTGATTTAAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 240
 |||||
 Db 485 CGCATTTGCAGAGATTAATTGATTTAAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 544
 |||||

QY 241 ATTCACCACATTTGGTGTG 258
 |||||
 Db 545 ATTCACCACATTTGGTGTG 562
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RESULT 20
 AX743954
 LOCUS AX743954 4457 bp DNA linear PAT 14-MAY-2003
 DEFINITION Sequence 2 from Patent WO03031630.
 ACCESSION AX743954
 VERSION AX743954.1 GI:30722651

KEYWORDS synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Fazio V., Rinaldi M., Sonzogni L., Tonon G. and Orsini G.
 TITLE Multi-cistronic vectors for gene transfer protocols
 JOURNAL Patent: WO 03031630-A 2 17-APR-2003;

FEATURES
 Keryos Spa (IT)
 source Location/Qualifiers
 1..4457
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 95.2%; Score 251.4; DB 6; Length 4457;
 Best Local Similarity 99.2%; Pred. No. 4.2e-62;
 Matches 263; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
 |||||
 Db 716 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 775
 |||||

QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
 |||||
 Db 776 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 835
 |||||

QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 180
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 Db 836 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 895
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QY 181 CGCATTTGCAGAGAT-ATTGATTTAAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 239
 |||||
 Db 896 CGCATTTGCAGAGATTAATTGATTTAAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 955
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QY 240 CATTCCACCATTTGGTGTGCACCTC 264
 |||||
 Db 956 CATTCCACCATTTGGTGTGCACCTC 980
 |||||

RESULT 21
 AX743956/c
 LOCUS AX743956 7334 bp DNA linear PAT 14-MAY-2003

DEFINITION Sequence 4 from Patent WO03031630.

ACCESSION AX743956
 VERSION AX743956.1 GI:30722653

KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Fazio V., Rinaldi M., Sonzogni L., Tonon G. and Orsini G.
 TITLE Multi-cistronic vectors for gene transfer protocols
 JOURNAL Patent: WO 03031630-A 4 17-APR-2003;

FEATURES
 Keryos Spa (IT)
 source Location/Qualifiers
 1..7334
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 95.2%; Score 251.4; DB 6; Length 7334;
 Best Local Similarity 99.2%; Pred. No. 3.9e-62;
 Matches 263; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
 |||||
 Db 2041 AATGTAGTCTTATGCAATACCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 1982
 |||||

QY 61 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
 |||||
 Db 1981 TGCCTTACAAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 1922
 |||||

QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 180
 |||||
 Db 1921 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAGCAACCACTAAATT 1862
 |||||

QY 181 CGCATTTGCAGAGAT-ATTGATTTAAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 239
 |||||
 Db 1861 CGCATTTGCAGAGATTAATTGATTTAAAGTGCCTAGCTCGATACAATAAAGCGCATTTGACC 1802
 |||||

QY 240 CATTCCACCATTTGGTGTGCACCTC 264
 |||||
 Db 1801 CATTCCACCATTTGGTGTGCACCTC 1777
 |||||

RESULT 22

ALVCG
 LOCUS ALVCG 7286 bp ss-RNA linear VRL 24-JUL-2000
 DEFINITION Avian leukemia virus ALV-RSA genome.

ACCESSION M37980
 VERSION M37980.1 GI:210272

KEYWORDS capsid protein; complete genome; envelope polypeptide; integrase;
 matrix protein; nucleocapsid protein; polymerase; protease; reverse
 transcriptase; surface protein; trans-acting factor; transmembrane
 protein.

SOURCE Avian leukosis virus
 ORGANISM Avian leukosis virus

REFERENCE 1 (bases 1 to 7286)
 AUTHORS Bieth E. and Darlix J.L.

TITLE Complete nucleotide sequence of a highly infectious avian leukosis
 virus
 JOURNAL Nucleic Acids Res. 20 (2), 367 (1992)
 MEDLINE 92158628
 PUBMED 1311072

COMMENT Draft entry and computer-readable sequence for [unpublished (1990)]
 kindly submitted
 by E. Bieth, 24-AUG-1990.

CREGC du CNRS
 118 route de Narbonne
 31062 Toulouse Cedex
 France.
 source Location/Qualifiers
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/organism="Avian leukosis virus"
/mol_type="genomic RNA"
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1..371
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22..101
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91..101
/note="5' imperfect repeat"
102..371
rpt_type=terminal
102..371
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102..120
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210..270
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218..248
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/db_xref="GI:210273"
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YLLIGVLVCEVTVGRADVHLLQEPGNLWITWANTQGTDFCLSTQSATSPFQCLLI
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MWDEHEQLQLGOSLPNTNTAQSIGITGCGPRPQGVWILGNSQCEATRFLLRH
PESKSTPEPTVTADRNHLFWGSEYCGAYGFNWXNCQGVQYRCGNARSRRPG
LBEICTRGCKWVNSQINESPFFTYNCTASLGNAGCCGKAGTILPERWVDS
TGSTCKRPAFLPAILICGDRWGGIPSRPVGGCYLGKJUTMLAPKHTDILKLVNS
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QANLTSLGDLDDVTSIRHAVIQNRAADIFLLAHGHCEDVAGMCCFNLSHSES
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372..2474
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/db_xref="GI:210274"
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817..876
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880..897
/gene="p2"
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/note="nucleocapsid protein"
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YEQLRGSDPNEAREWNLDMKMAWREIVQLSTTAALRNDPFLLEGAVARCEQAIGV
LGGSLTHPRCLWLFSTQPTKFTAWLEVLTLITKLASAVRTFGKVDIILLPAC
FREDLPLEGILLALRGFAGKIRSSDTPSIDLARPLHSLKVRVTDHPVGGTFTD
ASSTHKGVVVRREGSPRWIKIADLGASVQQLARAVAMALLWPTPTNVVDSAP
VAKLLKMGQGVSTAAAFILLEDALSORMAAVLHVSHSEVPGPTEGNVADSO
ATFQAYPREAKDLHTALHIGRALSKACNISMQQAREVVQTCPCNCSAPALEAGVP
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VLGRPKAITDNGSGCTSKSTREWLARGLAHTGTIPGNSQOQAVRBRNLLKDKIR
VLAEGDGFMKRIPTSQGLLAKAMALNHFERGTENTKPIQKHWRTVLTTEGPPVKI
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/note="reverse transcriptase beta-subunit"
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6261.6869 /bound_moiety="nucleocapsid"
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7037.7047 /note="3'imperfect repeat"
/rpt_type=terminal

ORIGIN

Query Match 94.1%; Score 248.4; DB 14; Length 7286;
Best Local Similarity 99.6%; Pred. No. 2.9e-61; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCTCTTATGCAATACCTCTTGTAGTCTTGGCAATGCTAAGGATGAGTACCAACA 60
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DB 7037 AATGAGCTCTTATGCAATACCTCTTGTAGTCTTGGCAATGCTAAGGATGAGTACCAACA 7096
|||||

QY 61 TGCCTTCAAGGAGAGAGAAAAGCAGCCGTCATGCGGATTTGGTGGAAAGTAAAGTGGTACGA 120
|||||
DB 7037 TGCCTTCAAGGAGAGAGAAAAGCAGCCGTCATGCGGATTTGGTGGAAAGTAAAGTGGTACGA 7156
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QY 121 TCGTGCCTTATTAGGAGGCAACAGAGCGGCTCTGACATGATTTGGACGACCACTAAATT 180
|||||
DB 7157 TCGTGCCTTATTAGGAGGCAACAGAGCGGCTCTGACATGATTTGGACGACCACTAAATT 7216
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QY 181 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGATGATCAATTAAGCGCATTTGACC 240
|||||
DB 7217 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGATGATCAATTAAGCGCATTTGACC 7276
|||||

QY 241 ATTACACACA 250
|||||
DB 7277 ATTACACACA 7286
|||||

RESULT 23
SYNRSV3MV
LOCUS SYNRSV3MV 3557 bp DNA circular SYN 27-APR-1993
DEFINITION Cloning vector RSV3.
ACCESSION M83240
VERSION M83240.1 GI:209303
KEYWORDS cDNA expression vector.
SOURCE unidentified cloning vector
ORGANISM unidentified cloning vector
REFERENCE 1 (sites)
AUTHORS Messing,J.
TITLE New M13 vectors for cloning
JOURNAL Meth. Enzymol. 101, 20-78 (1983)
MEDLINE 83296918
PUBMED 6310323
REFERENCE 2 (sites)
AUTHORS Gorman,C., Padmanabhan,R. and Howard,B.H.
TITLE High efficiency DNA-mediated transformation of primate cells
JOURNAL Science 221 (4610), 551-553 (1983)
MEDLINE 83249156
PUBMED 6306768
REFERENCE 3 (bases 1 to 3557)
AUTHORS Jacobson,S., Sekaly,R.P., Jacobson,C.L., McFarland,H.F. and Long,E.O.
TITLE HLA class II-restricted presentation of cytoplasmic measles virus antigens to cytotoxic T cells

JOURNAL J. Virol. 63 (4), 1756-1762 (1989)
MEDLINE 89178963
PUBMED 2784508
COMMENT Original source text: Cloning vector DNA.
FEATURES
source Location/Qualifiers
1..3557
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
misc_feature 1..29
/function="polylinker"
/evidence=experimental
misc_feature 912..3029
/function="ampicillin-resistance, replication origin"
/evidence=experimental
enhancer 3030..3557
/standard_name="5'LTR of Rous Sarcoma Virus"
/citation=[2]
/evidence=experimental

ORIGIN

Query Match 94.0%; Score 248.2; DB 12; Length 3557;
Best Local Similarity 98.5%; Pred. No. 3.7e-61; Indels 1; Gaps 1;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGAGCTCTTATGCAATACCTCTTGTAGTCTTGGCAATGCTAAGGATGAGTACCAACA 60
|||||
DB 3283 AATGAGCTCTTATGCAATACCTCTTGTAGTCTTGGCAATGCTAAGGATGAGTACCAACA 3348
|||||

QY 61 TGCCTTCAAGGAGAGAGAAAAGCAGCCGTCATGCGGATTTGGTGGAAAGTAAAGTGGTACGA 120
|||||
DB 3349 TGCCTTCAAGGAGAGAGAAAAGCAGCCGTCATGCGGATTTGGTGGAAAGTAAAGTGGTACGA 3408
|||||

QY 121 TCGTGCCTTATTAGGAGGCAACAGAGCGGCTCTGACATGATTTGGACGACCACTAAATT 180
|||||
DB 3409 TCGTGCCTTATTAGGAGGCAACAGAGCGGCTCTGACATGATTTGGACGACCACTAAATT 3468
|||||

QY 181 CGCATTTGCAGAGAT-ATTGATTTAAGTGCCTAGCTGATGATCAATTAAGCGCATTTGAC 239
|||||
DB 3469 CGCATTTGCAGAGAT-ATTGATTTAAGTGCCTAGCTGATGATCAATTAAGCGCATTTGAC 3528
|||||

QY 240 CATTCACACATTTGGTGGTGCACCTC 264
|||||
DB 3529 CATTCACACATTTGGTGGTGCACCTC 3553
|||||

RESULT 24
AR071324/c
LOCUS AR071324 4059 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 2 from patent US 5910488.
ACCESSION AR071324
VERSION AR071324.1 GI:7222212
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4059)
AUTHORS Nabel,G.J., Nabel,E.G., Lew,D. and Marquet,M.
TITLE Plasmids suitable for gene therapy
JOURNAL Patent: US 5910488-A 2 08-JUN-1999;
FEATURES Location/Qualifiers
source 1..4059
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 4059;
Best Local Similarity 98.5%; Pred. No. 3.6e-61; Indels 1; Gaps 1;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGAGCTCTTATGCAATACCTCTTGTAGTCTTGGCAATGCTAAGGATGAGTACCAACA 60
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DB 3156 AATGAGCTCTTATGCAATACCTCTTGTAGTCTTGGCAATGCTAAGGATGAGTACCAACA 3097
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QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGCTGAAGTAAGTGGTACGA 120
 Db 3096 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGCTGAAGTAAGTGGTACGA 3037
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAACCACTAAATT 180
 Db 3036 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGATTTGGAACCACTAAATT 2977
 QY 181 CCSCATTCAGAGAT-ATTGTTATTAGTGCCTAGCTCGATACATATTAAGCCATTTCAC 239
 Db 2976 CCSCATTCAGAGAT-ATTGTTATTAGTGCCTAGCTCGATACATATTAAGCCATTTCAC 2917
 QY 240 CATTCACCACATTTGGTGTGCACCTC 264
 Db 2916 CATTCACCACATTTGGTGTGCACCTC 2892

RESULT 25
 A38214
 LOCUS A38214 4341 bp DNA linear PAT 05-MAR-1997
 DEFINITION Sequence 58 from Patent WO9408008.
 ACCESSION A38214
 VERSION A38214.1 GI:2294819
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 4341)
 AUTHORS Hawkins,R.E., Russell,S.J., Stevenson,F.K. and Winter,G.P.
 TITLE IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
 JOURNAL MEDICAL RES COUNCIL (GB)
 COMMENT Patent: WO 9408008-A 58 14-APR-1994;
 Other publication CA 2145064 940414
 Other publication AU 4832493 940426
 Other publication JP 8501699T 960227.
 FEATURES
 source Location/Qualifiers
 1..4341
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match 94.0%; Score 248.2; DB 6; Length 4341;
 Best Local Similarity 98.5%; Pred. No. 3.6e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGATTAGCAACA 60
 Db 340 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGATTAGCAACA 399
 QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGCTGAAGTAAGTGGTACGA 120
 Db 400 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGCTGAAGTAAGTGGTACGA 459
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAACCACTAAATT 180
 Db 460 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGATTTGGAACCACTAAATT 519
 QY 181 CCSCATTCAGAGAT-ATTGTTATTAGTGCCTAGCTCGATACATATTAAGCCATTTCAC 239
 Db 520 CCSCATTCAGAGAT-ATTGTTATTAGTGCCTAGCTCGATACATATTAAGCCATTTCAC 2917
 QY 240 CATTCACCACATTTGGTGTGCACCTC 264
 Db 580 CATTCACCACATTTGGTGTGCACCTC 604

RESULT 26
 AX286570
 LOCUS AX286570 4341 bp DNA linear PAT 21-NOV-2001
 DEFINITION Sequence 1 from Patent WO0179510.
 ACCESSION AX286570

VERSION AX286570.1 GI:17048664
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Rice,J.H. and Stevenson,F.M.
 TITLE Materials and methods relating to immune responses to fusion proteins
 JOURNAL Patent: WO 0179510-A 1 25-OCT-2001;
 Cancer Research Ventures Limited (GB)
 FEATURES
 source Location/Qualifiers
 1..4341
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Vector pVACI"

ORIGIN
 Query Match 94.0%; Score 248.2; DB 6; Length 4341;
 Best Local Similarity 98.5%; Pred. No. 3.6e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGATTAGCAACA 60
 Db 340 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGCTTAACGATGATTAGCAACA 399
 QY 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGCTGAAGTAAGTGGTACGA 120
 Db 400 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCGATTGCTGAAGTAAGTGGTACGA 459
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATTTGGAACCACTAAATT 180
 Db 460 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGATTTGGAACCACTAAATT 519
 QY 181 CCSCATTCAGAGAT-ATTGTTATTAGTGCCTAGCTCGATACATATTAAGCCATTTCAC 239
 Db 520 CCSCATTCAGAGAT-ATTGTTATTAGTGCCTAGCTCGATACATATTAAGCCATTTCAC 579
 QY 240 CATTCACCACATTTGGTGTGCACCTC 264
 Db 580 CATTCACCACATTTGGTGTGCACCTC 604

RESULT 27
 SYNRSV5GPT
 LOCUS SYNRSV5GPT 4839 bp DNA circular SYN 16-MAR-2000
 DEFINITION Cloning vector RSV.5 (gpt).
 ACCESSION M83236
 VERSION M83236.1 GI:209304
 KEYWORDS cDNA expression vector.
 SOURCE Cloning vector pUC19
 ORGANISM Cloning vector pUC19
 artificial sequences; vectors.
 REFERENCE 1 (bases 1 to 4839)
 AUTHORS Long,E.O., Rosen-Bronson,S., Karp,D.R., Malnati,M., Sekaly,R.P. and Jaraquemada,D.
 TITLE Efficient cDNA expression vectors for stable and transient expression of HLA-DR in transfected fibroblast and lymphoid cells
 JOURNAL Hum. Immunol. 31 (4), 229-235 (1991)
 MEDLINE 92011006
 PUBMED 1655683
 FEATURES
 source Location/Qualifiers
 1..4839
 /organism="Cloning vector pUC19"
 /mol_type="genomic DNA"
 /db_xref="taxon:31851"
 /focus

source
 1..29
 /organism="Cloning vector pUC12"
 /mol_type="genomic DNA"
 /db_xref="taxon:83674"
 /note="HindIII to BamHI fragment of pUC12"

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30..872
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/notes="Bi-directional SV40 termination and
poly-adenylation sequences."
873..1929
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
1930..2273
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/notes="SV40 early promoter and origin of replication."
2274..4311
/organism="Cloning vector pBR322"
/mol_type="genomic DNA"
/db_xref="taxon:47470"
/notes="Ampicillin resistance gene and origin of replication
from the vector pBR322."
4312..4839
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11886"
/notes="5' long terminal repeat."
4840..5108
/function="polylinker"
/evidence=experimental
/product="guanine-hypoxanthine phosphoribosyltransferase"
/standard_name="gpt"
/notes="gpt gene from E.coli, putative mature peptide -
contains internal stop codons; putative"
2274..4311
/function="ampicillin resistance and origin of
replication"
/evidence=experimental

misc_feature
1..29
/function="polylinker"
/evidence=experimental

misc_feature
complement(873..1929)
/product="guanine-hypoxanthine phosphoribosyltransferase"
/standard_name="gpt"
/notes="gpt gene from E.coli, putative mature peptide -
contains internal stop codons; putative"

misc_feature
2274..4311
/function="ampicillin resistance and origin of
replication"
/evidence=experimental

ORIGIN

Query Match 94.0%; Score 248.2; DB 12; Length 4839;
Best Local Similarity 98.5%; Pred. No. 3.5e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGCTACTCTTATGCAATACCTCTGTAGTCTTGCACATGCTAAACGATGAGTTAGCAACA 60
Db |||||||TATGCAATACCTCTGTAGTCTTGCACATGCTAAACGATGAGTTAGCAACA 630
Qy 61 TGCCTTACAGGAGAGAAAAAGCACCGTCATGCCGATTTGGTGGAAAGTAAAGTGGTACGA 120
Db |||||||TGCCTTACAGGAGAGAAAAAGCACCGTCATGCCGATTTGGTGGAAAGTAAAGTGGTACGA 4690
Qy 121 TCGTGCCTTATAGGAGGACACAGCGGTCTGACATGCTTGGACGACACCACTAAATT 180
Db |||||||TCGTGCCTTATAGGAGGACACAGCGGTCTGACATGCTTGGACGACACCACTAAATT 4750
Qy 181 CGCATTGCAGAGAT-ATTGTATTATTAAGTGCCTTACGATACACATAAATACCCATTTGAC 239
Db |||||||CGCATTGCAGAGATATTGTATTATTAAGTGCCTTACGATACACATAAATACCCATTTGAC 4810
Qy 240 CATTACACACATTTGGTGTGCACCTC 264
Db |||||||CATTACACACATTTGGTGTGCACCTC 4835

RESULT 28
SYNRSVNEO
LOCUS 5108 bp DNA linear STN 06-APR-2001
DEFINITION cDNA expression vector RSV.5 (neo).
ACCESSION M83237
VERSION M83237.1 GI:209305
KEYWORDS cDNA expression vector.
SOURCE Expression vector RSV.5 (neo)

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ORGANISM Expression vector RSV.5(neo)
artificial sequences: vectors.
REFERENCE 1 (bases 1 to 5108)
AUTHORS Long,B.O., Roen-Bronson,S., Karp,D.R., Malnati,M., Sekaly,R.P. and
Jaraquemada,D.
TITLE Efficient cDNA expression vectors for stable and transient
expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE 92011006
PUBMED 1655683
FEATURES
Location/Qualifiers
1..5108
/organism="Expression vector RSV.5(neo)"
/mol_type="genomic DNA"
/db_xref="taxon:118308"
/focus
1..29
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/notes="HindIII to BamHI fragment of pUC12."
30..872
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/notes="Bi-directional SV40 termination and
poly-adenylation sequence."
873..879
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/notes="Remnant of gpt gene from the cDNA expression vector
RSV.5 (gpt)."
880..2197
/organism="Cloning vector pSV2neo"
/mol_type="genomic DNA"
/db_xref="taxon:31846"
/notes="TN5 neomycin-resistance gene from cloning vector
pSV2neo."
2198..2542
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/notes="SV40 early promoter and origin of replication."
2543..4580
/organism="Cloning vector pBR322"
/mol_type="genomic DNA"
/db_xref="taxon:47470"
/notes="Ampicillin resistance gene and origin of
replication from pBR322."
4581..5108
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11886"
/notes="5' long terminal repeat of Rous Sarcoma virus."
1..29
/function="polylinker"
/evidence=experimental
complement(880..2197)
/notes="neomycin resistance gene from pSV2neo, putative
mature peptide - contains internal stop codons; putative"
2543..4580
/product="ampicillin resistance"
/function="ampicillin resistance and origin of
replication"
/evidence=experimental
4581..5108
/standard_name="5'LTR of Rous Sarcoma Virus"
/function="promoter"
/evidence=experimental

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4581..5108

ORIGIN

Query Match 94.0%; Score 248.2; DB 12; Length 5108;

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CDS
/db_xref="Caxon:45196"
<13..480
/note="murine"
/citation={3}
/codon_start=1
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/transl_table=11
/product="T-cell receptor C beta 1"
/protein_id="AA072448.1"
/db_xref="GI:50524"
/translation="VDIANKQATVLCLAGFFPHVELSWWNGKEVGSVSTDFQA
KSGSYCLSRSLRYSAVFHNPENHFRCQVGHSEEDKWPGEKPTQNI SAE
AGRDCDGTIGSHVQSLATILLYELLCKATLYAVLSGILVMYKKNG"

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Query Match	94.0%;	Score	248.2;	DB	6;	Length	5653;
Best Local Similarity	98.5%;	Pred. No.	3.4e-61;				
Matches	261;	Conservative	0;	Mismatches	3;	Indels	1;
						Gaps	1;
QY	1	AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCACATGGTAAACGATGAGTTAGCAACA	60				
Db	340	AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCACATGGTAAACGATGAGTTAGCAACA	399				
QY	61	TGCCTTACAAGGAGAGAAAAGACACGGTGCATGCCCATTTGGTGAAGTGAAGTGGTGAAGA	120				
Db	400	TGCCTTACAAGGAGAGAAAAGACACGGTGCATGCCCATTTGGTGAAGTGAAGTGGTGAAGA	459				
QY	121	TGGTGCCTTTATTAGGACGGCAAACAGACGGGTCTGCATCGAATTGGACGAACCACTAAATT	180				
Db	460	TGGTGCCTTTATTAGGAGGGCAAACAGACAGTCTGCATGGAATTGGACGAACCACTGAATT	519				
QY	181	CGCANTGCAGAGAT-AATTGTATTAAAGTGGCTAGCTCGATACATAATAACGCCATTTGAC	239				
Db	520	CGCANTGCAGAGATAATTGTAATTTAAAGTGGCTAGCTCGATACATAATAACGCCATTTGAC	579				
QY	240	CAATCACCATTTGGTGTGCACCTC	264				
Db	580	CAATCACCATTTGGTGTGCACCTC	604				

RESULT 31			
I95540			
LOCUS	I95540	5853 bp	DNA linear PAT 01-DEC-1998

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DEFINITION Sequence 1 from patent US 5733543.
ACCESSION 195540
VERSION 195540.1 GI:3940010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 5653)
  Nabel,G.J., Woffendin,C., Yang,N.-S. and Sheehy,M.J.
  Introduction of HIV-protective genes into cells by
  particle-mediated gene transfer
  Patent: US 5733543-A 1 31-MAR-1998;
  FEATURES
    source
      1..5653
      /organism="unknown"
      /mol_type="unassigned DNA"
  ORIGIN
    Query Match 94.0%; Score 248.2; DB 6; Length 5653;
    Best Local Similarity 98.5%; Pred. No. 3.4e-61;
    Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
  Qy 1 AATGTAGTCTTATGCAATPACTTTGTAGTCTTTCGCAACATCGTAACGATGACTTAGCAACA 60
  Db 340 AATGTAGTCTTATGCAATPACTTTGTAGTCTTTCGCAACATCGTAACGATGACTTAGCAACA 399
  Qy 61 TGCCTTACAGAGAGAGAAAAGCAGCGTCGATCGATGCGATTTGGTGGAGTAAGGTGTACGA 120
  Db 400 TGCCTTACAGAGAGAGAAAAGCAGCGTCGATCGATGCGATTTGGTGGAGTAAGGTGTACGA 459
  Qy 121 TCGTGCCTTATTAGGAGGCAACAGCGGTCTGCATGATTTGGACGACCACTAAATT 180
  Db 460 TCGTGCCTTATTAGGAGGCAACAGCGGTCTGCATGATTTGGACGACCACTAAATT 519
  Qy 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTGCATACATAAAGCCCAATTGAC 239
  Db 520 CGCATTGCGAGAGATATTGTATTAAAGTGCCTAGCTGCATACATAAAGCCCAATTGAC 579
  Qy 240 CATTCCACCATTGGTGTGCACCTC 264
  Db 580 CATTCCACCATTGGTGTGCACCTC 604
  RESULT 32
  SYNPRSVNeo/c
  LOCUS SYNPRSVNeo 5736 bp DNA circular SYN 27-APR-1993
  DEFINITION PRSVNeo cloning vector for high efficiency gene transfer into mammalian cells.
  ACCESSION M77786
  VERSION M77786.1 GI:209147
  KEYWORDS
  SOURCE
  ORGANISM
  REFERENCE
    1 (bases 1 to 5736)
    Gilbert,W.
    Obtained from VecBase 3.0
  TITLE Unpublished (1991)
  JOURNAL
  COMMENT
    Original source text: Synthetic construct DNA.
    These data and their annotation were supplied to GenBank by Will
    Gilbert under the auspices of the GenBank Curator Program. PRSVNeo
    - Cloning Vector for High Efficiency Gene Transfer into Mammalian
    Cells
  ENTRY PRSVNeo #TYPE DNA CIRCULAR TITLE PRSVNeo -
  Cloning Vector for High Efficiency Gene Transfer
  into Mammalian Cells
  DATE 06-JUN-1986
  #sequence 16-DEC-1986
  ACCESSION V80064
  SOURCE artificial
  COLLECTION ATCC 37198
  REFERENCE
    number 1

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#authors Gorman C.
#book 'DNA cloning Volume II, a practical approach', pp.
143-190,
  edited by D. M. Glover, IRL Press, (1986),
  eds. D. Rickwood and B. D. Hames
COMMENT
  Entered by William Gilbert, Whitaker College, MIT, 02-APR-1986
  Revised 16-DEC-1986 by F. Pfeiffer:
  1012/3 'AT' to 'TA' to match revised sequence of PBR322 KEYWORDS
  CROSSREFERENCE
  #parent
    VecBase (3): PBR322, GenBank (50): SV4CG,
    GenBank (50): ALRPROL1B,
    GenBank (50): Trn5Neo, GenBank (50): Trn5IR1
  PARENT
    Features of PRSVNeo (5736 bp)
      residue source
      6- 529 550- 27 (c) Rous Sarcoma Virus (GenBank (50):
      ALRPROL1B)
      6- 529 3189-2667 (c) GenBank (50): ALRPROL1B (6 mutations)
      529-2644 2248-4363 PBR322
      2641-3634 1781-2774 SV40
      3631-4244 4100-4713 SV40
      4248-5533 1286- 1 (c) Trn5 (GenBank (50): TRNSNEO)
      5251-5736 1720-1235 (c) Trn5 (GenBank (50): TRNSIR1)
      Conflict (cfl) and Mutations (mut): none
  FEATURE
    1579-2367 789-1 (c) Ap-R; b-lactamase
    4589-5383 791-1 (c) Neo-R
  POLYLINKER
  SELECTION #resistance Ap
  SUMMARY PRSVNeo #length 5736 #checksum 3569.
  location/Qualifiers
  source
    1..5736
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
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    Query Match 94.0%; Score 248.2; DB 12; Length 5736;
    Best Local Similarity 98.5%; Pred. No. 3.4e-61;
    Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
  Qy 1 AATGTAGTCTTATGCAATPACTTTGTAGTCTTTCGCAACATCGTAACGATGACTTAGCAACA 60
  Db 269 AATGTAGTCTTATGCAATPACTTTGTAGTCTTTCGCAACATCGTAACGATGACTTAGCAACA 210
  Qy 61 TGCCTTACAGAGAGAGAAAAGCAGCGGTCTGCATGCGATTTGGTGGAGTAAGGTGTACGA 120
  Db 209 TGCCTTACAGAGAGAGAAAAGCAGCGGTCTGCATGCGATTTGGTGGAGTAAGGTGTACGA 150
  Qy 121 TCGTGCCTTATTAGGAGGCAACAGCGGTCTGCATGATTTGGACGACCACTAAATT 180
  Db 149 TCGTGCCTTATTAGGAGGCAACAGCGGTCTGCATGATTTGGACGACCACTAAATT 90
  Qy 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTGCATACATAAAGCCCAATTGAC 239
  Db 89 CGCATTGCGAGAGATATTGTATTAAAGTGCCTAGCTGCATACATAAAGCCCAATTGAC 30
  Qy 240 CATTCCACCATTGGTGTGCACCTC 264
  Db 29 CATTCCACCATTGGTGTGCACCTC 5
  RESULT 33
  AR215114
  LOCUS AR215114 6836 bp DNA linear PAT 25-SEP-2002
  DEFINITION Sequence 18 from patent US 6410266.
  ACCESSION AR215114
  VERSION AR215114.1 GI:23313242
  KEYWORDS
  SOURCE Unknown.
  ORGANISM Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 18 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..6836
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 6836;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGTTGAACGATGAGTTAGCAACA 60
Db 1558 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGTTGAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAAGTTAGCAACA 120
Db 1618 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAAGTTAGCAACA 1677
QY 121 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
Db 1678 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 1737
QY 161 CCCATTGCAGAGAT-ATTCTATTATTAAGTGGCTAGCTCGATACATATAAAGCCATTTGAC 239
Db 1738 CCCATTGCAGAGAT-ATTCTATTATTAAGTGGCTAGCTCGATACATATAAAGCCATTTGAC 1797
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1798 CATTACCAACATTTGGTGTGCACCTC 1822

RESULT 34
AR302356
LOCUS AR302356 6836 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 18 from patent US 6541221.
ACCESSION AR302356
VERSION AR302356.1 GI:31690610
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6541221-A 18 01-APR-2003;
FEATURES Location/Qualifiers
source 1..6836
/organism="unknown"
/mol_type="genomic DNA"

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Query Match 94.0%; Score 248.2; DB 6; Length 6836;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGTTGAACGATGAGTTAGCAACA 60
Db 1558 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGTTGAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAAGTTAGCAACA 120
Db 1618 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAAGTTAGCAACA 1677
QY 121 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
Db 1678 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 1737

QY 181 CGCATTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAATAAGCCATTTGAC 239
Db 1738 CGCATTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAATAAGCCATTTGAC 1797
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1798 CATTACCAACATTTGGTGTGCACCTC 1822

RESULT 35
AR373228
LOCUS AR373228 6836 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6602686.
ACCESSION AR373228
VERSION AR373228.1 GI:40075236
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 18 05-AUG-2003;
FEATURES Location/Qualifiers
source 1..6836
/organism="unknown"
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ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 6836;
Best Local Similarity 98.5%; Pred. No. 3.4e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAACATGTTGAACGATGAGTTAGCAACA 60
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QY 121 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 180
Db 1678 TCGTGCCTTATTAGAGAGCAACAGACGGGTCTGACATGGATTGGACGAACCACTAAATT 1737
QY 181 CGCATTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAATAAGCCATTTGAC 239
Db 1738 CGCATTGCAGAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAATAAGCCATTTGAC 1797
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1798 CATTACCAACATTTGGTGTGCACCTC 1822

RESULT 36
AR401614
LOCUS AR401614 6836 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6623958.
ACCESSION AR401614
VERSION AR401614.1 GI:40149062
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 18 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..6836

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QY	121	TGCGTGCCTTATTAGAGAGGCAACAGACACGGCTCTGACATGATTCGGACGACACCACTAAATT	180		
Db	1678	TGCGTGCCTTATTAGAGAGGCAACAGACACGGCTCTGACATGATTCGGACGACACCACTAAATT	1737		
QY	181	CGCATTTGCAGAGAT-ATTGTAATTTAAAGTGCCTAGCTCGATACAAATAAAGCCATTGAC	239		
Db	1738	CGCATTTGCAGAGATATTGTAATTTAAAGTGCCTAGCTCGATACAAATAAAGCCATTGAC	1797		
QY	240	CATTCAACACATTTGGTGTGCACCTC	264		
Db	1798	CATTCAACACATTTGGTGTGCACCTC	1822		
RESULT 38					
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LOCUS	XXU19931	6864 bp	DNA linear SYN 30-MAR-1995		
DEFINITION	Cloning vector pGlacRSV, complete sequence.				
ACCESSION	U19931				
VERSION	U19931.1	GI:644834			
KEYWORDS					
SOURCE	Cloning vector pGlacRSV				
ORGANISM	Cloning vector pGlacRSV				
REFERENCE	artificial sequences; vectors.				
AUTHORS	1 (bases 1 to 6864)				
TITLE	A versatile lacZ reporter vector				
JOURNAL	Unpublished				
AUTHORS	2 (bases 641 to 4011)				
TITLE	Ravid,K., Beeler,D.L., Rabin,M.S., Rulley,H.E. and Rosenberg,R.D.				
JOURNAL	Selective targeting of gene products with the megakaryocyte				
MEDLINE	Platelet factor 4 promoter				
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1521-1525 (1991)				
REFERENCE	91142205				
AUTHORS	1899930				
TITLE	3 (bases 1 to 6864)				
JOURNAL	Gottgens,B.B.				
FEATURES	Direct Submission				
source	Submitted (18-JAN-1995) Berthold B. Gottgens, Hematology, Cambridge University, MRC Centre, Hills Road, Cambridge, UK, CB2 2QH				
misc_feature	Location/Qualifiers				
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misc_feature	/organism="Cloning vector pGlacRSV"				
misc_feature	/mol_type="genomic DNA"				
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misc_feature	1..37				
misc_feature	/note="obtained from pGlac, Genbank Accession Number U19930"				
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misc_feature	632..6864				
misc_feature	/note="obtained from pGlac, Genbank Accession Number U19930"				
misc_feature	641..4011				
misc_feature	/note="obtained from pSDKlacZpa containing the E. coli lacZ gene followed by an SV40 polyA site"				
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CDS	/gene="lacZ"				
CDS	662..3727				
CDS	/gene="lacZ"				
CDS	/codon_start=1				
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CDS	/translation="MARDDPVVILQRDWNPGVQLMLAAHPFPAGWRNSEEARTRD				
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 QSLDRHVARFNDDFSFVLEAVQMGELRDVLTVSLWQGETVASSTAPFGHEI
 IBERGGYADRVTLKLVNPKWLSAIIPLNLYRAVELHTAGDTLIEACDCVDFREVR
 IENGLLNGRPLLIIRGVNRHPLHGQVNDQTVQDILIMKNFNNAVRCSHYPN
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 VIWLSIGNESGHGANHDALYRIKSVDPSPVQYEGGAD"ATADIIICPMYARVBDQ
 PFPAPVKSIIKWSLPLGSTRPLILCEVAHAMNSLGGFAKWOAFQYPRLOGGFVW
 DWVDSLLIKYDENGPNWSAGGDFGDTNDQRCMNGLVFADRTHEPALTEAKHQOQ
 FOPRLSGQTLIVTSEVLPFRSHNELLHMWALDGKPLASGEVPLDAPQKQLILEPE
 LPOPSAQQLWLVVVQPNATAMSEAGHISAMQWRNAENSLVLPASHAHFLHTT
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 DSGQGVATIVDEVSADTPHPARIGLNCOLAQVAERVNWGLGPOENYPRLTACPD
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 /translation="MSIQHFRVALIIPFPAARCLPVFAHPETLVKVKDAEDQLGARVGY
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ORIGIN

Query Match 94.0%; Score 248.2; DB 12; Length 6864;
 Best Local Similarity 98.5%; Pred. No. 3.4e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 60
 DB 365 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 424

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGTACGA 120
 DB 425 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGTACGA 484

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTGACATGATGATGAGCAACCACTAAAT 180
 DB 485 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTGACATGATGATGAGCAACCACTAAAT 544

QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTGATCGATACATAATAAACGCCATTGGAC 239
 DB 545 CGCATTTGCAGAGATATTGTATTATTAAGTGCCTGATCGATACATAATAAACGCCATTGGAC 604

QY 240 CATTCACCAACATTTGGTGTGCACCTC 264
 DB 605 CATTCACCAACATTTGGTGTGCACCTC 629

RESULT 39
 158322
 LOCUS I58322 8591 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 6 from patent US 5652092.
 ACCESSION I58322
 VERSION I58322.1 GI:2477560
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 Vitek, M. Peter, and Jacobsen, J. Steven.
 Amyloid precursor proteins and method of using same to assess
 agents which down-regulate formation of .beta.-amyloid peptide
 Patent: US 5652092-A 8 29-JUL-1997;
 Location/Qualifiers
 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 94.0%; Score 248.2; DB 6; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 3.3e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 5034

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGTACGA 120
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QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTGACATGATGATGAGCAACCACTAAAT 180
 DB 5095 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTGACATGATGATGAGCAACCACTAAAT 5154

QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTGATCGATACATAATAAACGCCATTGGAC 239
 DB 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTGATCGATACATAATAAACGCCATTGGAC 239

TITLE Amyloid precursor proteins and method of using same to assess
 agents which down-regulate formation of .beta.-amyloid peptide
 JOURNAL Patent: US 5652092-A 6 29-JUL-1997;
 FEATURES Location/Qualifiers
 source 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 3.3e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 5034

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGTACGA 120
 DB 5035 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGTACGA 5094

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTGACATGATGATGAGCAACCACTAAAT 180
 DB 5095 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTGACATGATGATGAGCAACCACTAAAT 5154

QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTGATCGATACATAATAAACGCCATTGGAC 239
 DB 5155 CGCATTTGCAGAGATATTGTATTATTAAGTGCCTGATCGATACATAATAAACGCCATTGGAC 5214

QY 240 CATTCACCAACATTTGGTGTGCACCTC 264
 DB 5215 CATTCACCAACATTTGGTGTGCACCTC 5239

RESULT 40
 158323
 LOCUS I58323 8591 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 8 from patent US 5652092.
 ACCESSION I58323
 VERSION I58323.1 GI:2477561
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 Vitek, M. Peter, and Jacobsen, J. Steven.
 Amyloid precursor proteins and method of using same to assess
 agents which down-regulate formation of .beta.-amyloid peptide
 Patent: US 5652092-A 8 29-JUL-1997;
 Location/Qualifiers
 1..8591
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 94.0%; Score 248.2; DB 6; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 3.3e-61;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGATGATGAGTTAGCAACA 5034

QY 61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGTACGA 120
 DB 5035 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTTGGTGAAGTAAGGTGTACGA 5094

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTGACATGATGATGAGCAACCACTAAAT 180
 DB 5095 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTGACATGATGATGAGCAACCACTAAAT 5154

QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTGATCGATACATAATAAACGCCATTGGAC 239
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Query Match	94.0%;	Score 248.2;	DB 6;	Length 8591;
Best Local Similarity	98.5%;	Pred. No. 3.3e-61;		
Matches 261;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;
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QY	1	AATGTAGCTCTTATGCAATACACTCTTCTTTAGTCTTTGCAACATGTTAACAAGTATGATTTAGCAACA	60	
DB	4975	AATGTAGCTCTTATGCAATACACTCTTCTTTAGTCTTTGCAACATGTTAACAAGTATGATTTAGCAACA	5034	
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QY	61	TGCCTTACAGGAGAGAAAGACACCGTGCAATCCGATTCGGATTTGGTGGAGTTAAGTGGTTACGA	120	
DB	5035	TGCCTTACAGGAGAGAAAGACACCGTGCAATCCGATTCGGATTTGGTGGAGTTAAGTGGTTACGA	5094	
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QY	121	TGCTGCCCTTATTAGGAAAGCAACAGACGGGCTTGACATGCGATTGGACGAACCACTAAATTT	180	
DB	5095	TGCTGCCCTTATTAGGAAAGCAACAGACGGGCTTGACATGCGATTGGACGAACCACTAAATTT	5154	
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QY	181	CGCATTTGCGAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATATAAGCCCAATTGCAC	239	
DB	5155	CGCATTTGCGAGATTAATTGTATTTAAGTGGCTAGCTCGATACATATAAGCCCAATTGCAC	5214	
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QY	240	CATTCCACCACATTTGGTGTGCACCTC	264	
DB	5215	CATTCCACCACATTTGGTGTGCACCTC	5239	
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RESULT 43				
LOCUS	I77052	8591 bp	DNA	linear PAT 03-APR-1998
DEFINITION	Sequence 6 from patent US 5693478.			
ACCESSION	I77052			
VERSION	I77052.1	GI:3013206		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 8591)			
AUTHORS	Vitek M.Peter, and Jacobsen J.Steven.			
TITLE	Method of detecting amyloid precursor proteins			
JOURNAL	Patent: US 5693478-A 6 02-DEC-1997;			
FEATURES	Location/Qualifiers			
source	1..8591			
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ORIGIN				
Query Match	94.0%;	Score 248.2;	DB 6;	Length 8591;
Best Local Similarity	98.5%;	Pred. No. 3.3e-61;		
Matches 261;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;
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QY	1	AATGTAGCTCTTATGCAATACACTCTTGTAGTCTTTGCAACATGTTAACAAGTATGATTTAGCAACA	60	
DB	4975	AATGTAGCTCTTATGCAATACACTCTTGTAGTCTTTGCAACATGTTAACAAGTATGATTTAGCAACA	5034	
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QY	61	TGCCTTACAGGAGAGAAAGACACCGTGCAATCCGATTCGGATTTGGTGGAGTTAAGTGGTTACGA	120	
DB	5035	TGCCTTACAGGAGAGAAAGACACCGTGCAATCCGATTCGGATTTGGTGGAGTTAAGTGGTTACGA	5094	
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QY	121	TGCTGCCCTTATTAGGAAAGCAACAGACGGGCTTGACATGCGATTGGACGAACCACTAAATTT	180	
DB	5095	TGCTGCCCTTATTAGGAAAGCAACAGACGGGCTTGACATGCGATTGGACGAACCACTAAATTT	5154	
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QY	181	CGCATTTGCGAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATATAAGCCCAATTGCAC	239	
DB	5155	CGCATTTGCGAGATTAATTGTATTTAAGTGGCTAGCTCGATACATATAAGCCCAATTGCAC	5214	
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QY	240	CATTCCACCACATTTGGTGTGCACCTC	264	
DB	5215	CATTCCACCACATTTGGTGTGCACCTC	5239	
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LOCUS       I77053               8591 bp      DNA      linear      PAT 03-APR-1998
DEFINITION   Sequence 8 from patent US 5693478.
ACCESSION   I77053
VERSION     I77053.1  GI:3013207
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 8591)
AUTHORS     Vitek M.Peter. and Jacobsen,J.Steven.
TITLE       Method of detecting amyloid precursor proteins
JOURNAL     Patent: US 5693478-A 8 02-DEC-1997;
FEATURES
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ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 8591;
Best Local Similarity 98.5%; Pred. No. 3.3e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGCTAAGATGAGTTAGCAACA 60
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QY 61 TGCCTTACAGGAGAGAAAAGAACCCGTCATGCGGATTTGGTGAAGTAAGTGTACGA 120
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QY 121 TCGTGCCTTATTAGAAGCAACAGACGGGCTGACATGATTTGACGAAACCACTAAATT 180
Db 5095 TCGTGCCTTATTAGAAGCAACAGACGGGCTGACATGATTTGACGAAACCACTAAATT 5154

QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGATACATATAAACCCATTGAC 239
Db 5155 CGCATTTGCAGAGATTAATTGTATTATTAAGTGCCTAGCTCGATACATATAAACCCATTGAC 5214

QY 240 CATTCACCACATTTGGTGTGCACCTC 264
Db 5215 CATTCACCACATTTGGTGTGCACCTC 5239

ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 8591;
Best Local Similarity 98.5%; Pred. No. 3.3e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGCTAAGATGAGTTAGCAACA 60
Db 4975 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGCTAAGATGAGTTAGCAACA 5034

QY 61 TGCCTTACAGGAGAGAAAAGAACCCGTCATGCGGATTTGGTGAAGTAAGTGTACGA 120
Db 5035 TGCCTTACAGGAGAGAAAAGAACCCGTCATGCGGATTTGGTGAAGTAAGTGTACGA 5094

QY 121 TCGTGCCTTATTAGAAGCAACAGACGGGCTGACATGATTTGACGAAACCACTAAATT 180
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QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGATACATATAAACCCATTGAC 239
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QY 240 CATTCACCACATTTGGTGTGCACCTC 264
Db 5215 CATTCACCACATTTGGTGTGCACCTC 5239

ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 8591;
Best Local Similarity 98.5%; Pred. No. 3.3e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGCTAAGATGAGTTAGCAACA 60
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QY 61 TGCCTTACAGGAGAGAAAAGAACCCGTCATGCGGATTTGGTGAAGTAAGTGTACGA 120

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Db 5035 TGCCTTACAGGAGAGAAAAGAACCCGTCATGCGGATTTGGTGAAGTAAGTGTACGA 5094

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QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGATACATATAAACCCATTGAC 239
Db 5155 CGCATTTGCAGAGATTAATTGTATTATTAAGTGCCTAGCTCGATACATATAAACCCATTGAC 5214

QY 240 CATTCACCACATTTGGTGTGCACCTC 264
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RESULT 46
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LOCUS       I87174               8591 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION   Sequence 8 from patent US 5703209.
ACCESSION   I87174
VERSION     I87174.1  GI:3206892
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 8591)
AUTHORS     Vitek M.Peter. and Jacobsen,J.Steven.
TITLE       Amyloid precursor proteins and method of using same to assess
             agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL     Patent: US 5703209-A 8 30-DEC-1997;
FEATURES
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ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 8591;
Best Local Similarity 98.5%; Pred. No. 3.3e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGCTAAGATGAGTTAGCAACA 60
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QY 61 TGCCTTACAGGAGAGAAAAGAACCCGTCATGCGGATTTGGTGAAGTAAGTGTACGA 120
Db 5035 TGCCTTACAGGAGAGAAAAGAACCCGTCATGCGGATTTGGTGAAGTAAGTGTACGA 5094

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Db 5095 TCGTGCCTTATTAGAAGCAACAGACGGGCTGACATGATTTGACGAAACCACTAAATT 5154

QY 181 CGCATTTGCAGAGAT-ATTGTATTATTAAGTGCCTAGCTCGATACATATAAACCCATTGAC 239
Db 5155 CGCATTTGCAGAGATTAATTGTATTATTAAGTGCCTAGCTCGATACATATAAACCCATTGAC 5214

QY 240 CATTCACCACATTTGGTGTGCACCTC 264
Db 5215 CATTCACCACATTTGGTGTGCACCTC 5239

RESULT 47
187174
LOCUS       AR215118            9737 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION   Sequence 22 from patent US 6410266.
ACCESSION   AR215118
VERSION     AR215118.1  GI:23313246
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 9737)

```

AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 22 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAAGGAGAGAAAAAGCACCGTCATGCGATTTGGTGAAGTAAGTGTGTACGA 120
Db 1471 TGCCTTACAAGGAGAGAAAAAGCACCGTCATGCGATTTGGTGAAGTAAGTGTGTACGA 1530

Qy 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGCTGATGAGTAAGCAACCACTAAATT 180
Db 1531 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGCTGATGAGTAAGCAACCACTAAATT 1590

Qy 181 CGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 239
Db 1591 CGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 1650

Qy 240 CATTCACACATTTGGTGTGCACCTC 264
Db 1651 CATTCACACATTTGGTGTGCACCTC 1675

RESULT 48
AR215119
LOCUS AR215119 9737 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 23 from patent US 6410266.
ACCESSION AR215119
VERSION AR215119.1 GI:23313247
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 23 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAAGGAGAGAAAAAGCACCGTCATGCGATTTGGTGAAGTAAGTGTGTACGA 120
Db 1471 TGCCTTACAAGGAGAGAAAAAGCACCGTCATGCGATTTGGTGAAGTAAGTGTGTACGA 1530

Qy 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGCTGATGAGTAAGCAACCACTAAATT 180
Db 1531 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGCTGATGAGTAAGCAACCACTAAATT 1590

Qy 181 CGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 239

Db 1591 CGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 1650

Qy 240 CATTCACACATTTGGTGTGCACCTC 264
Db 1651 CATTCACACATTTGGTGTGCACCTC 1675

RESULT 49
AR215124
LOCUS AR215124 9737 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 28 from patent US 6410266.
ACCESSION AR215124
VERSION AR215124.1 GI:23313252
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 28 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATCTTTGTAGTCTTGTGCAACATGCTAAACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAAGGAGAGAAAAAGCACCGTCATGCGATTTGGTGAAGTAAGTGTGTACGA 120
Db 1471 TGCCTTACAAGGAGAGAAAAAGCACCGTCATGCGATTTGGTGAAGTAAGTGTGTACGA 1530

Qy 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGCTGATGAGTAAGCAACCACTAAATT 180
Db 1531 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGCTGATGAGTAAGCAACCACTAAATT 1590

Qy 181 CGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 239
Db 1591 CGCATTGCAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAAACGCCATTTGAC 1650

Qy 240 CATTCACACATTTGGTGTGCACCTC 264
Db 1651 CATTCACACATTTGGTGTGCACCTC 1675

RESULT 50
AR302360
LOCUS AR302360 9737 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 22 from patent US 6541221.
ACCESSION AR302360
VERSION AR302360.1 GI:31690614
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6541221-A 22 01-APR-2003;
FEATURES Location/Qualifiers
source 1..9737
/organism="unknown"
/mol_type="genomic DNA"

Query Match	94.0%;	Score 248.2;	DB 6;	Length 9737;
Best Local Similarity	98.5%;	Pred. No. 3.2e-61;		
Matches 261;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;
1	AATGAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAATCGGTACAGATGAGTTAGCAACA	60		
1411	AATGAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAATCGGTAAACGATGAGTTAGCAACA	1470		
61	TGCGCTTACAGGAGAGAAAAGACACCGTGCAATGCCGATTTGGTGGAGTAGGTGCTACGA	120		
1471	TGCGCTTACAGGAGAGAAAAGACACCGTGCAATGCCGATTTGGTGGAGTAGGTGCTACGA	1530		
121	TCGTGCCCTTATTAGGAGGCGAACAGACGGGCTCGACATCGATTGGAGCAACACATAAATT	180		
1531	TCGTGCCCTTATTAGGAGGCGAACAGACGGGCTCGACATCGATTGGAGCAACACATAAATT	1590		
181	CGCATTTGCAGAGAT-ATTGTTATTAAAGTGGCTAGCTTCGATCAACAATAAAGCCCATTTGAC	239		
1591	CGCATTTGCAGAGATAATTGTATTATGTTGGCTAGCTCGATACATAATAAGCCCATTTGAC	1650		
240	CATTCAACCATTTGGTGGACCTC	264		
1651	CATTCAACCATTTGGTGGACCTC	1675		

Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. NO. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
1 AAGTGTAGTCTTATGCATTACTCTTCTAGCTTTCGACACATGGTAACGATGAGTTAGCAACA 60

Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 120

Db 1471 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 1530

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGTCTGACATGGATTGGACGAACCACTAAATT 180

Db 1531 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTGAATT 1590

QY 181 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 239

Db 1591 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 1650

QY 240 CATTCAACCATTTGGTGGACCTC 264

Db 1651 CATTCAACCATTTGGTGGACCTC 1675

RESULT 54

AR373233

LOCUS AR373233 9737 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 23 from patent US 6602686.

ACCESSION AR373233

VERSION AR373233.1 GI:40075241

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 9737)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and method for non-targeted activation of endogenous genes

JOURNAL Patent: US 6602686-A 23 05-AUG-2003;

FEATURES

source

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;

Best Local Similarity 98.5%; Pred. No. 3.2e-61;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 60

Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 120

Db 1471 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 1530

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGTCTGACATGGATTGGACGAACCACTAAATT 180

Db 1531 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTGAATT 1590

QY 181 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 239

Db 1591 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 1650

QY 240 CATTCAACCATTTGGTGGACCTC 264

Db 1651 CATTCAACCATTTGGTGGACCTC 1675

RESULT 55

AR373238

LOCUS AR373238 9737 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 28 from patent US 6602686.

ACCESSION AR373238

VERSION AR373238.1 GI:40075246

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 9737)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and method for non-targeted activation of endogenous genes

JOURNAL Patent: US 6602686-A 23 05-AUG-2003;

FEATURES

source

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;

Best Local Similarity 98.5%; Pred. No. 3.2e-61;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 60

Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 120

Db 1471 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 1530

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGTCTGACATGGATTGGACGAACCACTAAATT 180

Db 1531 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTGAATT 1590

QY 181 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 239

Db 1591 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 1650

QY 240 CATTCAACCATTTGGTGGACCTC 264

Db 1651 CATTCAACCATTTGGTGGACCTC 1675

RESULT 56

AR401618

LOCUS AR401618 9737 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 22 from patent US 6623958.

ACCESSION AR401618

VERSION AR401618.1 GI:40149066

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 9737)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and methods for non-targeted activation of endogenous genes

JOURNAL Patent: US 6623958-A 22 23-SEP-2003;

FEATURES

source

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;

Best Local Similarity 98.5%; Pred. No. 3.2e-61;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 60

Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 120

Db 1471 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 1530

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGTCTGACATGGATTGGACGAACCACTAAATT 180

Db 1531 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTGAATT 1590

QY 181 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 239

Db 1591 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 1650

QY 240 CATTCAACCATTTGGTGGACCTC 264

Db 1651 CATTCAACCATTTGGTGGACCTC 1675

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 9737)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and method for non-targeted activation of endogenous genes

JOURNAL Patent: US 6602686-A 28 05-AUG-2003;

FEATURES

source

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/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;

Best Local Similarity 98.5%; Pred. No. 3.2e-61;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 60

Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 120

Db 1471 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 1530

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGTCTGACATGGATTGGACGAACCACTAAATT 180

Db 1531 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTGAATT 1590

QY 181 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 239

Db 1591 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 1650

QY 240 CATTCAACCATTTGGTGGACCTC 264

Db 1651 CATTCAACCATTTGGTGGACCTC 1675

RESULT 56

AR401618

LOCUS AR401618 9737 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 22 from patent US 6623958.

ACCESSION AR401618

VERSION AR401618.1 GI:40149066

KEYWORDS

SOURCE

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 9737)

AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.

TITLE Compositions and methods for non-targeted activation of endogenous genes

JOURNAL Patent: US 6623958-A 22 23-SEP-2003;

FEATURES

source

1. .9737

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 94.0%; Score 248.2; DB 6; Length 9737;

Best Local Similarity 98.5%; Pred. No. 3.2e-61;

Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 60

Db 1411 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 120

Db 1471 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 1530

QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGTCTGACATGGATTGGACGAACCACTAAATT 180

Db 1531 TCGTGCCTTATTAGGAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTGAATT 1590

QY 181 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 239

Db 1591 CCGCATTCAGAGAT-ATTGTATTAAAGTGGCTAGCTCGATACATAAACCCTATTGAC 1650

QY 240 CATTCAACCATTTGGTGGACCTC 264

Db 1651 CATTCAACCATTTGGTGGACCTC 1675

Db 1531 TCGTGCTTTATTAGGAAGGCAACAGACAGAGTCTGCATGGAATTGGACGAACCACTGAATT 1590

Qy 181 CCGCATTGCAGAGAT-ATTGTTATTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 239
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Db 1591 CCGCATTGCAGAGATTAATTGTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 1650
|||||

Qy 240 CATTACCAACATTGGTGTGCACCTC 264
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Db 1651 CATTACCAACATTGGTGTGCACCTC 1675

RESULT 57
AR401619
LOCUS AR401619 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6623958.
ACCESSION AR401619
VERSION AR401619.1 GI:40149067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and Methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 23-SEP-2003;
FEATURES
source Location/Qualifiers
1. .9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACCTCTGTAGTCTTGCATGGAATTGGACGAACCACTGAATT 60
Db 1411 AATGTAGTCTTATGCAATACATTTGTATTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 1470
Qy 61 TGCCTTACAGGAGAGAAAGACCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAGACCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 1530
Qy 121 TCGTGCTTTATTAGGAAGGCAACAGACAGCGGTCTGCATGGAATTGGACGAACCACTGAATT 180
Db 1531 TCGTGCTTTATTAGGAAGGCAACAGACAGCGGTCTGCATGGAATTGGACGAACCACTGAATT 1590
Qy 181 CCGCATTGCAGAGAT-ATTGTTATTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 239
Db 1591 CCGCATTGCAGAGATTAATTGTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 1650

RESULT 59
AR215120
LOCUS AR215120 9871 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 24 from patent US 6410266.
ACCESSION AR215120
VERSION AR215120.1 GI:23313248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9871)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and Methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 24-25-JUN-2002;
FEATURES
source Location/Qualifiers
1. .9871
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9871;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACCTCTGTAGTCTTGCATGGAATTGGACGAACCACTGAATT 60
Db 1545 AATGTAGTCTTATGCAATACATTTGTATTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 1604
Qy 61 TGCCTTACAGGAGAGAAAGACCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 120
Db 1605 TGCCTTACAGGAGAGAAAGACCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 1664
Qy 121 TCGTGCTTTATTAGGAAGGCAACAGACAGCGGTCTGCATGGAATTGGACGAACCACTGAATT 180
Db 1665 TCGTGCTTTATTAGGAAGGCAACAGACAGCGGTCTGCATGGAATTGGACGAACCACTGAATT 1724
Qy 181 CCGCATTGCAGAGAT-ATTGTTATTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 239
Db 1725 CCGCATTGCAGAGATTAATTGTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 1784
Qy 240 CATTACCAACATTGGTGTGCACCTC 264
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source 1. .9737
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9737;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACCTCTGTAGTCTTGCATGGAATTGGACGAACCACTGAATT 60
Db 1411 AATGTAGTCTTATGCAATACATTTGTATTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 1470
Qy 61 TGCCTTACAGGAGAGAAAGACCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAGACCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 1530
Qy 121 TCGTGCTTTATTAGGAAGGCAACAGACAGCGGTCTGCATGGAATTGGACGAACCACTGAATT 180
Db 1531 TCGTGCTTTATTAGGAAGGCAACAGACAGCGGTCTGCATGGAATTGGACGAACCACTGAATT 1590
Qy 181 CCGCATTGCAGAGAT-ATTGTTATTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 239
Db 1591 CCGCATTGCAGAGATTAATTGTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 1650

RESULT 59
AR215120
LOCUS AR215120 9871 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 24 from patent US 6410266.
ACCESSION AR215120
VERSION AR215120.1 GI:23313248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9871)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and Methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 24-25-JUN-2002;
FEATURES
source Location/Qualifiers
1. .9871
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 94.0%; Score 248.2; DB 6; Length 9871;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACCTCTGTAGTCTTGCATGGAATTGGACGAACCACTGAATT 60
Db 1545 AATGTAGTCTTATGCAATACATTTGTATTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 1604
Qy 61 TGCCTTACAGGAGAGAAAGACCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 120
Db 1605 TGCCTTACAGGAGAGAAAGACCGTGCATGCGGATGCTGGAAGTAAGTGGTACGA 1664
Qy 121 TCGTGCTTTATTAGGAAGGCAACAGACAGCGGTCTGCATGGAATTGGACGAACCACTGAATT 180
Db 1665 TCGTGCTTTATTAGGAAGGCAACAGACAGCGGTCTGCATGGAATTGGACGAACCACTGAATT 1724
Qy 181 CCGCATTGCAGAGAT-ATTGTTATTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 239
Db 1725 CCGCATTGCAGAGATTAATTGTTAAAGTGCCTAGCTCGATACATTAAGCCATTGTGAC 1784
Qy 240 CATTACCAACATTGGTGTGCACCTC 264
|||||

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Db      1785 CATTCAACCACTTGGTGTGCACCTC 1809

RESULT 60
AR302362
LOCUS      AR302362      9871 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 24 from patent US 6541221.
ACCESSION AR302362
VERSION    AR302362.1 GI:31690616
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 9871)
AUTHORS     Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE       Compositions and methods for non-targeted activation of endogenous
            genes
JOURNAL     Patent: US 6541221-A 24 01-APR-2003;
FEATURES     Location/Qualifiers
             source
               1..9871
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 9871;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 AATGTAGCTCTTATGCAATACACTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 60
Db      1545 AATGTAGCTCTTATGCAATACACTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 1604

Qy      61 TGCCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 120
Db      1605 TGCCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 1664

Qy      121 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGATTTGGACGACCACTAAATT 180
Db      1665 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGATTTGGACGACCACTAAATT 1724

Qy      181 CGCATTTGCAGAGAT-ATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 239
Db      1725 CGCATTTGCAGAGATATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 1784

Qy      240 CATTCAACCACTTGGTGTGCACCTC 264
Db      1785 CATTCAACCACTTGGTGTGCACCTC 1809

RESULT 62
AR401620
LOCUS      AR401620      9871 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 24 from patent US 6623958.
ACCESSION AR401620
VERSION    AR401620.1 GI:40149068
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 9871)
AUTHORS     Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE       Compositions and methods for non-targeted activation of endogenous
            genes
JOURNAL     Patent: US 6623958-A 24 23-SEP-2003;
FEATURES     Location/Qualifiers
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Query Match      94.0%; Score 248.2; DB 6; Length 9871;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 AATGTAGCTCTTATGCAATACACTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 60
Db      1545 AATGTAGCTCTTATGCAATACACTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 1604

Qy      61 TGCCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 120
Db      1605 TGCCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 1664

Qy      121 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGATTTGGACGACCACTAAATT 180
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Qy      181 CGCATTTGCAGAGAT-ATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 239
Db      1725 CGCATTTGCAGAGATATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 1784

Qy      240 CATTCAACCACTTGGTGTGCACCTC 264
Db      1785 CATTCAACCACTTGGTGTGCACCTC 1809

RESULT 63
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LOCUS      AR215121      10060 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION Sequence 25 from patent US 6410266.
ACCESSION AR215121

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Qy      1 AATGTAGCTCTTATGCAATACACTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 60
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Qy      61 TGCCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 120
Db      1605 TGCCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 1664

Qy      121 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGATTTGGACGACCACTAAATT 180
Db      1665 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGATTTGGACGACCACTAAATT 1724

Qy      181 CGCATTTGCAGAGAT-ATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 239
Db      1725 CGCATTTGCAGAGATATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 1784

Qy      240 CATTCAACCACTTGGTGTGCACCTC 264
Db      1785 CATTCAACCACTTGGTGTGCACCTC 1809

RESULT 62
AR401620
LOCUS      AR401620      9871 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 24 from patent US 6623958.
ACCESSION AR401620
VERSION    AR401620.1 GI:40149068
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 9871)
AUTHORS     Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE       Compositions and methods for non-targeted activation of endogenous
            genes
JOURNAL     Patent: US 6623958-A 24 23-SEP-2003;
FEATURES     Location/Qualifiers
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ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 9871;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy      1 AATGTAGCTCTTATGCAATACACTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 60
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Qy      61 TGCCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 120
Db      1605 TGCCTTTACAAGGAGAGAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGGTACGA 1664

Qy      121 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGATTTGGACGACCACTAAATT 180
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Qy      181 CGCATTTGCAGAGAT-ATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 239
Db      1725 CGCATTTGCAGAGATATTGTATTATTAAAGTGCCTAGCTCGATACATAATAAAGCCATTTCAC 1784

Qy      240 CATTCAACCACTTGGTGTGCACCTC 264
Db      1785 CATTCAACCACTTGGTGTGCACCTC 1809

RESULT 63
AR215121
LOCUS      AR215121      10060 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION Sequence 25 from patent US 6410266.
ACCESSION AR215121

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VERSION      AR215121.1  GI:23313249
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10060)
AUTHORS      Harrington,J.J., and Rundlett,S.
TITLE        Compositions and methods for non-targeted activation of endogenous
              genes
JOURNAL      Patent: US 6410266-A 25 JUN-2002;
FEATURES     Location/Qualifiers
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ORIGIN
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Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTAACGATGAGTTAGCAACA 60
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QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGCTGCGATGCGATTGGTGGAGTAAGTGGTACGA 120
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QY 121 TCGTGCTTATTAGGAGGCAACAGACCGGCTGACATGATTTGGACCAACCACTAAATT 180
DB 1854 TCGTGCTTATTAGGAGGCAACAGACCGGCTGACATGATTTGGACCAACCACTAAATT 1913

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QY 240 CATTCACCACTTGGTGTGCACCTC 264
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QY 1 AATGTAGCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTAACGATGAGTTAGCAACA 60
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QY 240 CATTCACCACTTGGTGTGCACCTC 264
DB 1974 CATTCACCACTTGGTGTGCACCTC 1998

ORIGIN
Query Match      94.0%; Score 248.2; DB 6; Length 10060;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTAACGATGAGTTAGCAACA 60
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Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTAACGATGAGTTAGCAACA 60
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QY 121 TCGTGCTTATTAGGAGGCAACAGACCGGCTGACATGCTTAACGATGAGTTAGCAACA 180
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QY 240 CATTCACCACTTGGTGTGCACCTC 264
DB 1974 CATTCACCACTTGGTGTGCACCTC 1998

RESULT 65
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LOCUS      AR373235
DEFINITION Sequence 25 from patent US 6602686.
ACCESSION AR373235
VERSION    AR373235.1  GI:40075243
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10060)
AUTHORS     Harrington,J.J., Sherf, B. and Rundlett,S.
TITLE       Compositions and method for non-targeted activation of endogenous
              genes
JOURNAL     Patent: US 6602686-A 25 05-AUG-2003;
FEATURES    Location/Qualifiers
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Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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DB 1914 CCGCATTGCAGAGAT-ATTGTATTAAAGTCCCTAGCTCGATACATAAAGCCATTGGAC 1973

QY 240 CATTCACCACTTGGTGTGCACCTC 264
DB 1974 CATTCACCACTTGGTGTGCACCTC 1998

RESULT 66
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LOCUS      AR401621
DEFINITION Sequence 25 from patent US 6623958.
ACCESSION AR401621
VERSION    AR401621.1  GI:40149069
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10060)
AUTHORS     Harrington,J.J., Sherf, B. and Rundlett,S.
TITLE       Compositions and methods for non-targeted activation of endogenous
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JOURNAL Patent: US 6623959-A 25 SEP-2003;
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Best local similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      1  AATGTAGTCTTATGCAATACTCTTGTTAGTCTTGCAACATGCTGAACGATGAGTTAGCAACA 60
Db      1734  AATGTAGTCTTATGCAATACACTTGTTAGTCTTGCAACATGCTGAACGATGAGTTAGCAACA 1793

QY      61  TGCCTTACAGGAGAGAAAGAACACCGCTGCATGCGCATTTGGTGGAAAGTAAAGTGGTACGA 120
Db      1794  TGCCTTACAGGAGAGAAAGAACACCGCTGCATGCGCATTTGGTGGAAAGTAAAGTGGTACGA 1853

QY      121  TCGTGCCTTATTAGGAGGCAACAGACGGGCTGACATGTCATGTCATGTCATGTCATGTCATGTCAT 180
Db      1854  TCGTGCCTTATTAGGAGGCAACAGACGGTCTGACATGTCATGTCATGTCATGTCATGTCATGTCAT 1913

QY      181  CGCGATTCAGAGAT-ATTGTATTAAAGTGCTAGCTGCATACATTAAGCCCATTTGCAC 239
Db      1914  CGCATTCGACAGATAATTGTATTAAAGTGCTAGCTGCATACATTAAGCCCATTTGCAC 1973

QY      240  GATTCCACCATTTGGTGTGCACCTC 264
Db      1974  GATTCCACCATTTGGTGTGCACCTC 1998

RESULT 67
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Cloning vector pDR2, complete sequence.
U02428
U02428.1  GI:413794

Cloning vector pDR2
Cloning vector pDR2
artificial sequences; vectors.
Murphy,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.
cDNA expression cloning in human cells using the plambdadr2
episomal vector system
Methods: A Companion to Methods in Enzymology 4, 111-131 (1992)
2 (bases 1 to 10737)
Kitts,P.A.
CLONTECH Vectors On Disc version 1.3
Unpublished
3 (bases 1 to 10737)
Kitts,P.A.
Direct Submission
Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
1020 East Meadow Circle, Palo Alto, CA 94303, USA
This vector can be obtained from CLONTECH Laboratories, Inc., 1020
East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
call (415) 424-8222 or (800) 662-2566, extension 1. International
customers, please contact your local distributor. For technical
information, call (415) 424- 8222 or (800) 662-2566, extension 3.
This sequence has been compiled from information in the sequence
databases, published literature and other sources, together with
partial sequences obtained by CLONTECH; this vector has not been
completely sequenced. If you suspect there is an error in this
sequence, please contact CLONTECH's Technical Service Department at
(415) 424-8222 or (800) 662-2566, extension 3 or E-mail
TECH@CLONTECH.COM.

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Db 527 TCGTGCCTTATTAGGAAGGCAACAGACGCGGTCTGACATGATTTGGACGAACCACTAAATT 586
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Db 587 CCGCATTTGCAGAGATATTGTATTAAAGTCCCTAGCTCGATACATATAAAGCCCATTTGAC 646
QY 240 CATTACACCATTTGGTGTGCACCTC 264
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RESULT 69
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LOCUS 11265 bp DNA circular PAT 20-SEP-2000
DEFINITION Sequence 1 from Patent WO9844129.
ACCESSION AX031159
VERSION AX031159.1 GI:10278512
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Lew,A.M., Boyle,J.S. and Brady,J.L.
TITLE Enhancement of immune response using targeting molecules
JOURNAL INST MEDICAL W & E HALL (AU) ; QUEENSLAND INST MED RES (AU) ; CSL
LTD (AU) ; LEW ANDREW MARK (AU) ; UNIV MELBOURNE (AU) ; BOYLE
JEFFREY STEPHEN (AU) ; BRADY JAMIE LOUISE (AU) ; COMM SCIENT IND
RES ORG (AU)

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Best Local Similarity 98.5%; Pred. No. 3.2e-61;
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Db 489 TCGTGCCTTATTAGGAAGGCAACAGACGCGGTCTGACATGATTTGGACGAACCACTAAATT 548
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QY 240 CATTACACCATTTGGTGTGCACCTC 264
Db 609 CATTACACCATTTGGTGTGCACCTC 633

RESULT 70
AX665480
LOCUS 16958 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 3 from Patent WO03002735.
ACCESSION AX665480
VERSION AX665480.1 GI:29290565
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Lancotot,C., Gingras,R. and Gaumond,M.-H.

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LOCUS BD084805
DEFINITION Enhancement of immune response using targeting molecules.
ACCESSION BD084805
VERSION BD084805.1 GI:22630415
KEYWORDS JP 2001522235-A/1.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 11265)
AUTHORS Boyle,J.S., Brady,J.L. and Lew,A.M.
TITLE Enhancement of immune response using targeting molecules
JOURNAL Patent: JP 2001522235-A 1 13-NOV-2001.
THE COUNCIL OF THE QUEENSLAND INSTITUTE OF MEDICAL RESEARCH, THE
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, THE
UNIVERSITY OF MELBOURNE, THE WALTER AND ELIZA HALL INSTITUTE OF
MEDICAL RESEARCH, CSL LTD
OS Unidentified
PN JP 2001522235-A/1
PD 13-NOV-2001
PF 26-MAR-1998 JP 1998540989
PR 27-MAR-1997 AU POS891,13-FEB-1998 AU PP 1830 PI
JEFFREY STEPHEN BOYLE, JAMIE LOUISE BRADY, ANDREW MARK LEW PC
C12N15/62, C07K19/00, A61K39/00, A61K48/00
CC Strandedness: Double;
CC Topology: Circular;
CC Enhancement of immune response using targeting molecules PH
Key source Location/Qualifiers
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Query Match 94.0%; Score 248.2; DB 6; Length 11265;
Best Local Similarity 98.5%; Pred. No. 3.2e-61;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
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Db 429 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCCGATTTGTCGAGTAAAGTGGTAGCA 488
QY 121 TCGTGCCTTATTAGGAAGGCAACAGACGCGGTCTGACATGATTTGGACGAACCACTAAATT 180
Db 489 TCGTGCCTTATTAGGAAGGCAACAGACGCGGTCTGACATGATTTGGACGAACCACTAAATT 548
QY 181 CCGCATTTGCAGAGAT-ATTGTATTAAAGTCCCTAGCTCGATACATATAAAGCCCATTTGAC 239
Db 549 CCGCATTTGCAGAGATATTGTATTAAAGTCCCTAGCTCGATACATATAAAGCCCATTTGAC 608
QY 240 CATTACACCATTTGGTGTGCACCTC 264
Db 609 CATTACACCATTTGGTGTGCACCTC 633

RESULT 71
AX665480
LOCUS 16958 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 3 from Patent WO03002735.
ACCESSION AX665480
VERSION AX665480.1 GI:29290565
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Lancotot,C., Gingras,R. and Gaumond,M.-H.

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Best local similarity 98.5%; Pred. No. 8.9e-61;
Matches 260; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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		DEFINITION	Cellular immunogens useful cancer vaccines.				
		ACCESSION	BD005483				
		VERSION	BD005483.1	GI:18633854			

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Job time : 1480.54 secs

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		DEFINITION	Cellular immunogens useful cancer vaccines.				
		ACCESSION	BD005483				
		VERSION	BD005483.1	GI:18633854			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 03:02:06 ; Search time 227.972 Seconds
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Title: US-09-733-368a-1_COPY_349_612

Perfect score: 264

Sequence: 1 aatgtagtcttatgcaatac.....accacattggtgcaactc 264

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373663 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
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8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	262.4	99.4	2829	3 AAH43951	Aah43951 Rous sarc
4	262.4	99.4	2878	3 AAH43951	Aah43951 Rous sarc
5	262.4	99.4	3310	3 AAH43951	Aah43951 Rous sarc
6	262.4	99.4	3311	3 AAH43951	Aah43951 Rous sarc
7	262.4	99.4	3385	4 AAH43951	Aah43951 Rous sarc
8	262.4	99.4	4487	3 AAH43951	Aah43951 Rous sarc
9	262.4	99.4	7086	9 AAH43951	Aah43951 Rous sarc
10	262.4	99.4	8238	3 AAH43951	Aah43951 Rous sarc
11	262.4	99.4	33622	8 AAH43951	Aah43951 Rous sarc
12	262.4	99.4	34302	3 AAH43951	Aah43951 Rous sarc
13	262.4	99.4	35211	8 AAH43951	Aah43951 Rous sarc
14	261.4	99.0	11627	3 AAH43951	Aah43951 Rous sarc
15	260.4	98.6	2245	7 AAH43951	Aah43951 Rous sarc
16	259.2	98.2	5177	2 AAH43951	Aah43951 Rous sarc
17	257.6	97.6	4965	2 AAH43951	Aah43951 Rous sarc
18	257.2	97.4	262	4 AAH43951	Aah43951 Rous sarc
19	256.4	97.1	562	7 AAH43951	Aah43951 Rous sarc
20	251.4	95.2	7334	9 AAH43951	Aah43951 Rous sarc
21	251.4	95.2	7334	9 AAH43951	Aah43951 Rous sarc
22	248.2	94.0	397	3 AAH43951	Aah43951 Rous sarc
23	248.2	94.0	397	3 AAH43951	Aah43951 Rous sarc

24	248.2	94.0	397	3	AAZ93077	Aaz93077 Rous Sarc
25	248.2	94.0	4059	2	AAQ75974	Aaq75974 pHLA-B7 e
26	248.2	94.0	4341	2	AAQ62391	Aaq62391 Vector pv
27	248.2	94.0	4341	6	AAH17704	Aah17704 Vector pv
28	248.2	94.0	4341	6	ABN83143	Abn83143 Plasmid p
29	248.2	94.0	5653	2	AAT02998	Aat02998 RSV tar R
30	248.2	94.0	5653	2	AAT76802	Aat76802 RSV tar R
31	248.2	94.0	5750	2	AAQ43814	Aaq43814 pRLD3D4 C
32	248.2	94.0	6207	2	AAQ43813	Aaq43813 pRLD2D3D4 C
33	248.2	94.0	6274	2	AAQ43812	Aaq43812 pRLD1D2D3
34	248.2	94.0	6838	3	AAAS3869	Aaas3869 Expressio
35	248.2	94.0	8591	2	AAT84562	Aat84562 Plasmid p
36	248.2	94.0	8591	2	AAT84561	Aat84561 Plasmid p
37	248.2	94.0	8591	2	AAT87083	Aat87083 Plasmid p
38	248.2	94.0	8591	2	AAT87084	Aat87084 Plasmid p
39	248.2	94.0	8591	2	AAV04866	Aav04866 cDNA enco
40	248.2	94.0	8591	2	AAV04865	Aav04865 cDNA enco
41	248.2	94.0	8591	2	AAV05850	Aav05850 APP-REP 7
42	248.2	94.0	8591	2	AAV05849	Aav05849 APP-REP 7
43	248.2	94.0	8902	6	ABL57333	Ab157333 Vector pl
44	248.2	94.0	9725	3	AAAS3873	Aaas3873 Expressio
45	248.2	94.0	9722	3	AAAS3879	Aaas3879 Expressio
46	248.2	94.0	9738	3	AAAS3874	Aaas3874 Expressio
47	248.2	94.0	9873	3	AAAS3875	Aaas3875 Expressio
48	248.2	94.0	10054	3	AAAS3876	Aaas3876 Expressio
49	248.2	94.0	11265	7	AAV59501	Aav59501 Plasmid p
50	248.2	94.0	16958	7	AAV55269	Aal55269 DNA of ex
51	248.2	94.0	37808	2	AAZ02780	Aaz02780 Vector pM
52	247.2	93.6	7223	2	AAT62602	Aat62602 Luciferas
53	244.8	92.7	565	2	AAT71261	Aat71261 Rous sarc
54	244.8	92.7	565	3	AAZ60824	Aaz60824 Nucleotid
55	232	87.9	5130	6	AAZ28311	Aaz28311 LSRNL vec
56	232	87.9	7170	6	AAZ28272	Aaz28272 LSRNL vec
57	217.4	82.3	10468	8	ACD27899	AcD27899 pdmT2 vec
58	213	80.7	3188	2	AAQ6310	Aaq6310 Sequence
59	213	80.7	3276	2	AAQ6311	Aaq6311 Sequence
60	213	80.7	3383	2	AAQ6309	Aaq6309 Sequence
61	213	80.7	3427	2	AAQ6313	Aaq6313 Sequence
62	213	80.7	3979	2	AAQ6312	Aaq6312 Sequence
63	211.6	80.2	858	5	AAZ92489	Aaz92489 Fragment
64	205.2	77.7	9542	2	AAZ77359	Aaz77359 Polynucle
65	205.2	77.7	9542	3	AAZ90391	Aaz90391 987Bneuo
66	205.2	77.7	11282	2	AAZ27850	Aaz27850 Complete
67	205.2	77.7	11282	4	AAZ04741	Aaz04741 Alphavira
68	205.2	77.7	11282	5	AAZ84024	Aaf84024 Complete
69	187.6	71.1	5283	6	ABK10062	Abk10062 Expressio
70	174.2	66.0	4993	7	AAZ53272	Aaz53272 MESV2/EGF
71	174.2	66.0	5843	7	AAZ53270	Aaz53270 MESV2/ACT
72	174.2	66.0	5843	7	AAZ53271	Aaz53271 MESV2/IRE
73	174.2	66.0	6250	4	AAZ14296	Aad14296 MESV/EGF
74	174.2	66.0	6250	5	AAZ13899	Aad13899 Recombina
75	173.4	65.7	11500	3	AAZ59077	Aaz59077 Nucleotid
76	173.4	65.7	11500	6	ABA94279	AbA94279 Nucleotid
77	173.4	65.7	11500	8	AAZ56865	Aal56865 DNA seque
78	173.4	65.7	11500	9	AAZ53274	Aad53274 Chromosom
79	171.8	65.1	4374	7	AAZ53273	Aad53273 MESV2/EGF
80	171.8	65.1	5047	7	AAZ53290	Aad53290 MESV2/EGF
81	171.8	65.1	5074	7	AAZ53291	Aad53291 MESV2/EGF
82	171.8	65.1	5097	7	AAZ53292	Aad53292 MESV2/EGF
83	171.8	65.1	5119	7	AAZ53273	Aad53273 MESV2/EGF
84	171.8	65.1	5217	7	AAZ53289	Aad53289 MESV2/EGF
85	171.8	65.1	5340	7	AAZ53291	Aad53291 MESV2/EGF
86	171.8	65.1	6279	4	AAZ14199	Aad14199 MESV/EGF
87	171.8	65.1	8513	6	AAZ14203	Aad14203 MESV/EGF
88	161.2	61.1	766	6	AB190071	Ab190071 Human pol
89	142.4	53.9	211	6	AB159286	Ab159286 Nucleotid
90	139.8	53.0	213	6	AB159285	Ab159285 Nucleotid
91	139.8	53.0	213	6	AB159276	Ab159276 Nucleotid
92	127.8	48.4	210	6	AB159280	Ab159280 Nucleotid
93	109.4	41.4	194	6	AB159277	Ab159277 Nucleotid
94	103.4	39.2	178	6	AB159284	Ab159284 Nucleotid
95	102.4	38.8	178	6	AB159283	Ab159283 Nucleotid
96	102.2	38.7	181	6	AB159278	Ab159278 Nucleotid

97	93.8	35.5	97	6	AB159281	Nuc.leotid
98	88	33.3	101	4	AA84457	Rous sarc
99	87	33.0	92	6	AB159282	Nuc.leotid
100	82.6	31.3	149	6	AB159279	Nuc.leotid

ATTACHMENTS

RESULT 1	
AAH43951	
ID	AAH43951 standard; DNA; 648 BP.
XX	
AC	AAH43951;
XX	
DT	06-SEP-2001 (first entry)
XX	
DE	Rous sarcoma virus promoter nucleotide sequence SEQ ID NO:1.
XX	
KW	Rous sarcoma virus; promoter; enhancer; RSV; primate; gene expression;
KN	transgene; genetic engineering; gene therapy; immunisation; ds.
XX	
OS	Rous sarcoma virus.
XX	
PN	W0200142444-A2.
XX	
PD	14-JUN-2001.
XX	
PF	08-DEC-2000; 2000WO-US033256.
XX	
PR	10-DEC-1999; 99US-0170019P.
XX	
PA	(ARIA-) ARIAD GENE THERAPEUTICS INC.
PA	(UYPE-) UNIV PENNSYLVANIA.
PI	Rivera V, Zoltick P, Wilson JM;
XX	
DR	WPI; 2001-381673/40.
XX	
PT	Genetically engineering a primate for expression of a desired gene,
PT	comprises introducing into the primate a transgene comprising Rous
PT	Sarcoma virus (RSV) promoter and a nucleic acid sequence heterologous to
PT	RSV promoter.
XX	
PS	Claim 7: Page 44: 64bp; English.

Db	349	AAATGAGCTTATGCAATACCTTTGTAGTCTTTGCAACATGCTAACGATGAGTTAGCAACA	408
QY	61	TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAGGTGCTACGA	120
Db	409	TGCTTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGGAAAGTAAGGTGCTACGA	468
QY	121	TGTGCTCTATTAGGAAGGCAACAGAGGGCTCTGCATCGAATTGGACGAACCACTAAATT	180
Db	469	TGTGCTCTATTAGGAAGGCAACAGAGGGCTCTGCATCGAATTGGACGAACCACTAAATT	528
QY	181	CGCATGTCAGACATATTGTATTTTAAGTGCCTAGCTCGATACAATAAAGCCATTGGACC	240
Db	529	CGCATGTCAGACATATTGTATTTTAAGTGCCTAGCTCGATACAATAAAGCCATTGGACC	588
QY	241	ATTCAACACATTTGGTGTGACCTC	264
Db	589	ATTCAACACATTTGGTGTGACCTC	612
RESULT 2			
AA14722			
ID	AA14722 standard; DNA; 2187 BP.		
XX	AAA14722;		
XX	AC		
XX	06-AUG-2003 (revised)		
DT	08-AUG-2000 (first entry)		
DT			
XX			
DE	Nucleotide sequence of region A of vector Ad5RSVbeta-lactamase.		
XX			
KW	Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;		
KW	replication-deficient adenovirus type 5; suicide gene therapy;		
KW	cancer cell; chemotherapy; beta-lactamase prodrug enzyme; prodrug TCM;		
KW	anticancer; tumor; leukemia; breast cancer; Wilm's tumor;		
KW	small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;		
KW	papillary adenocarcinoma; ss.		
XX			
OS	Synthetic.		
OS	Rous sarcoma virus.		
OS	Mastadenovirus.		
XX			
XX	WO20020608-A1.		
FN			
PD	13-APR-2000.		
PF			
PF	01-OCT-1999; 95WO-USC020908.		
PR	02-OCT-1998; 96US-00165321.		
XX	(GENO-) GENOTHERAPEUTICS INC.		
PA			
PI	Steiner MS;		
XX	WPI; 2000-303788/26.		
DR			
PT	Treating cancer using viral vectors which encode enzymes that convert		
PT	inactive drugs to active cytotoxic agents, expression of the enzyme is		
PT	tissue specific therefore targeting the effects of the drug to tumor		
PT	cells.		
XX			
PS	Disclosure; Fig 10; 130pp; English.		
CC			
CC	The specification describes a method for inducing cellular cytotoxicity		
CC	in tumor cells using replication-deficient adenovirus type 5 expression		
CC	vectors. The vectors comprise a sequence encoding a beta-lactamase under		
CC	the control of a Rous Sarcoma virus in combination with a prodrug		
CC	conjugated to a toxic agent. Tissue specific expression of the enzyme		
CC	converts the inactive drugs into active cancer killing agents. The		
CC	adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-		
CC	lactamase sequence is inserted within this region. The vectors are used		
CC	for suicide gene therapy. This involves introducing genes into cancer		
CC	cells that encode enzymes capable of converting inactive drugs into		


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XX 04-SEP-1998; 98US-00148275.
XX (GENO-) GENOTHERAPEUTICS INC.
XX Steiner MS, Lu Y;
XX WPI; 2000-257001/22.
XX Replication-deficient adenovirus type 5 expression vectors used for gene
XX therapy of cancer, especially prostate cancer, comprising an insertion of
XX nucleic acid encoding cytochrome p450 genes.
XX Claim 17; Fig 11B; 110pp; English.
XX Replication-deficient adenovirus type 5 expression vectors comprise an
XX adenovirus genome with a deletion in the E1 and E2 region of the genome
XX and an insertion within the region under the control of a Rous Sarcoma
XX Virus promoter can be used to induce chemotoxicity in tumour cells. Three
XX such expression vectors are described, the inserted nucleic acids in each
XX being the following: Vector (I) has an insertion of a nucleic acid
XX encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-
XX 2628). Vector (II) has an insertion of a nucleic acid encoding a
XX cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector
XX (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
XX dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
XX designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
XX can be induced by administering (I) and (III) or (II) and (III) into the
XX tumor cell (e.g. a prostate tumor cell) to selectively sensitise the cell
XX to a prodrug and then administering the prodrug which kills the cell,
XX inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
XX therapy to transfer a drug susceptibility gene to the tumor which
XX activates a nontoxic prodrug intratumorally so the released drug can kill
XX the tumor cells containing the drug susceptibility gene. This sequence is
XX designated region A of the vector Ad5RSV3A4 and is the sequence of the
XX cytochrome 3A4 p450
XX
XX Sequence 2878 BP; 786 A; 609 C; 710 G; 773 T; 0 U; 0 Other;
XX
Query Match 99.4%; Score 262.4; DB 3; Length 2878;
Best Local Similarity 99.6%; Pred. No. 1.6e-81;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 AANTGAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGCTAAGCATGAGTATGACCA 60
Db |||||
Db 541 AANTGAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGCTAAGCATGAGTATGACCA 600
QY 61 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCGGATGCTGCAATGCTGGAAGTAAAGTGTACGA 120
Db |||||
Db 601 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCGGATGCTGCAATGCTGGAAGTAAAGTGTACGA 660
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGATGACCAACCACTAAATT 180
Db |||||
Db 661 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGATGACCAACCACTAAATT 720
QY 181 CCGCATTCGAGAGATATTGATTTAAGTGCCTAGCTGATACATAAAGCCATTGACC 240
Db |||||
Db 721 CCGCATTCGAGAGATATTGATTTAAGTGCCTAGCTGATACATAAAGCCATTGACC 780
QY 241 ATTCACCAATTGGTGTGCACCTC 264
Db |||||
Db 781 ATTCACCAATTGGTGTGCACCTC 804
XX
RESULT 5
AAZ93331
ID AAZ93331 standard; DNA; 3310 BP.
XX
XX AAZ93331;
XX AC
XX AC
XX 04-JUL-2000 (first entry)
XX
XX Partial sequence of replication deficient adenoviral vector Ad5RSVRed.

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XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
XX Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
XX prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
XX Synthetic.
XX W0200014256-A1.
XX 16-MAR-2000.
XX 03-SEP-1999; 99WO-US018834.
XX 04-SEP-1998; 98US-00148275.
XX (GENO-) GENOTHERAPEUTICS INC.
XX Steiner MS, Lu Y;
XX WPI; 2000-257001/22.
XX Replication-deficient adenovirus type 5 expression vectors used for gene
XX therapy of cancer, especially prostate cancer, comprising an insertion of
XX nucleic acid encoding cytochrome p450 genes.
XX Disclosure; Fig 10; 110pp; English.
XX Replication-deficient adenovirus type 5 expression vectors comprise an
XX adenovirus genome with a deletion in the E1 and E2 region of the genome
XX and an insertion within the region under the control of a Rous Sarcoma
XX Virus promoter can be used to induce chemotoxicity in tumour cells. Three
XX such expression vectors are described, the inserted nucleic acids in each
XX being the following: Vector (I) has an insertion of a nucleic acid
XX encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-
XX 2628). Vector (II) has an insertion of a nucleic acid encoding a
XX cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector
XX (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
XX dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
XX designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
XX can be induced by administering (I) and (III) or (II) and (III) into the
XX tumor cell (e.g. a prostate tumor cell) to selectively sensitise the cell
XX to a prodrug and then administering the prodrug which kills the cell,
XX inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
XX therapy to transfer a drug susceptibility gene to the tumor which
XX activates a nontoxic prodrug intratumorally so the released drug can kill
XX the tumor cells containing the drug susceptibility gene. This sequence is
XX designated region A of the vector Ad5RSVRed
XX
XX Sequence 3310 BP; 755 A; 881 C; 980 G; 694 T; 0 U; 0 Other;
XX
Query Match 99.4%; Score 262.4; DB 3; Length 3310;
Best Local Similarity 99.6%; Pred. No. 1.7e-81;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 AANTGAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGCTAAGCATGAGTATGACCA 60
Db |||||
Db 541 AANTGAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGCTAAGCATGAGTATGACCA 600
QY 61 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCGGATGCTGCAATGCTGGAAGTAAAGTGTACGA 120
Db |||||
Db 601 TGCCTTACAGGAGAGAAAAGCAACCGTGCATGCGGATGCTGCAATGCTGGAAGTAAAGTGTACGA 660
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGATGACCAACCACTAAATT 180
Db |||||
Db 661 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGACATGATGATGACCAACCACTAAATT 720
QY 181 CCGCATTCGAGAGATATTGATTTAAGTGCCTAGCTGATACATAAAGCCATTGACC 240
Db |||||
Db 721 CCGCATTCGAGAGATATTGATTTAAGTGCCTAGCTGATACATAAAGCCATTGACC 780
QY 241 ATTCACCAATTGGTGTGCACCTC 264
Db |||||
Db 781 ATTCACCAATTGGTGTGCACCTC 804
XX

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RESULT 6
AA293079
ID AA293079 standard; DNA; 3311 BP.
XX
AC
AA293079;
XX
DT 04-JUL-2000 (first entry)
XX
DE Partial sequence of replication deficient adenoviral vector AdRSVRred.
XX
KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
XX
OS Synthetic.
XX
FN WO200014256-A1.
XX
PD 16-MAR-2000.
XX
PF 03-SEP-1999; 99WO-US018934.
XX
PR 04-SEP-1998; 98US-00148275.
XX
PA (GENC-) GENOTHERAPEUTICS INC.
XX
PI Steiner MS, Lu Y;
XX
XX WPI; 2000-257001/22.
XX
PT Replication-deficient adenovirus type 5 expression vectors used for gene
PT therapy of cancer, especially prostate cancer, comprising an insertion of
PT nucleic acid encoding cytochrome p450 genes.
XX
PS Claim 18; Fig 11C; 110pp; English.
XX
CC Replication-deficient adenovirus type 5 expression vectors comprise an
CC adenovirus genome with a deletion in the E1 and E2 region of the genome
CC and an insertion within the region under the control of a Rous Sarcoma
CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three
CC such expression vectors are described, the inserted nucleic acids in each
CC being the following: Vector (I) has an insertion of a nucleic acid
CC encoding a cytochrome 2C9 p450 and is designated AdRSRV2C9 (ATCC VR-
CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
CC cytochrome 3A4 p450 and is designated AdRSRV3A4 (ATCC VR-2629). Vector
CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
CC designated AdRSVRred (ATCC VR-2630). The chemotoxicity of a tumor cell
CC can be induced by administering (I) and (III) or (II) and (III) into the
CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell
CC to a prodrug and then administering the prodrug which kills the cell,
CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
CC therapy to transfer a drug susceptibility gene to the tumor which
CC activates a nontoxic prodrug intratumorally so the released drug can kill
CC the tumor cells containing the drug susceptibility gene. This sequence is
CC designated region A of the vector AdRSVRred and is the sequence of the
CC cytochrome NADPH p450 reductase
XX
SQ Sequence 3311 BP; 755 A; 981 C; 981 G; 694 T; 0 U; 0 Other;

Query Match 99.4%; Score 262.4; DB 3; Length 3311;
Best Local Similarity 99.6%; Pred. No. 1.7e-81;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTGCAATGTTAGTACCA 60
DB 541 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAGTACCA 600
QY 61 TGCCTTACAAGAGAGAAAAGACCGTGCATGCCGATGGTGGAGTACGTTAGTACGA 120
DB 601 TGCCTTACAAGAGAGAAAAGACCGTGCATGCCGATGGTGGAGTACGTTAGTACGA 660

QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGGCTCTGACATGGATTGGACGACCACTAAATT 180
DB 661 TCGTGCCCTTATTAGGAGGCAACAGACGGGCTCTGACATGGATTGGACGACCACTAAATT 720
QY 181 CGCATTTGCAGAGATATTGTATTATTTAAGTGCCTTAGCTGATACATAAAGCGCATTGACC 240
DB 721 CGCATTTGCAGAGATATTGTATTATTTAAGTGCCTTAGCTGATACATAAAGCGCATTGACC 780
QY 241 ATTCACCAATTGGTGTGCACCTC 264
DB 781 ATTCACCAATTGGTGTGCACCTC 804
RESULT 7
AAC89169
ID AAC89169 standard; DNA; 3885 BP.
XX
AC AAC89169;
XX
DT 08-MAR-2001 (first entry)
XX
DE AdRSVpHYDE region A coding sequence.
XX
KW p-HYDE; cytostatic; gene therapy; apoptosis; leukaemia; prostate;
KW tumour suppressor gene; DNA repair; cancer; melanoma; lymphoma;
KW colorectal; pancreatic; breast; brain; gastric carcinoma; ds.
XX
OS Unidentified.
XX
FN WO200071564-A2.
XX
PD 30-NOV-2000.
XX
PF 01-MAY-2000; 2000WO-US011456.
XX
PR 29-APR-1999; 99US-00302457.
PR 29-APR-1999; 99US-0131607P.
PR 08-FEB-2000; 2000US-00499817.
XX
XX (UYTE-) UNIV TENNESSEE RES CORP.
XX
XX Steiner MS, Wang C, Rinaldy A, Menon R;
XX WPI; 2001-032016/04.
XX
XX New isolated nucleic acid encoding a mammalian p-Hyde protein of the p-
XX Hyde family is useful for treating cancer, e.g. prostate cancer.
XX
XX Disclosure; Fig 10; 171pp; English.
XX
XX The present sequence is region A of AdRSVpHYDE. AdRSVpHYDE is an
XX adenovirus vector expressing p-HYDE. p-HYDE induces susceptibility of a
XX cancer cell to cell death. The p-HYDE gene is associated with the
XX regression of tumour growth in vivo, the induction to susceptibility to
XX apoptosis caused by UV or chemotherapy induced DNA damage and prevention
XX of DNA repair with the upregulation of apoptosis as the result of UV
XX damage and the failure to repair DNA. The present sequence may be used to
XX treat cancer, preferably melanoma, lymphoma, leukaemia, prostate,
XX colorectal, pancreatic, breast, brain or gastric carcinoma
XX
SQ Sequence 3885 BP; 847 A; 1039 C; 1063 G; 936 T; 0 U; 0 Other;

Query Match 99.4%; Score 262.4; DB 4; Length 3885;
Best Local Similarity 99.6%; Pred. No. 1.8e-81;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAGTACCACTAGTACCA 60
DB 541 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAGTACCACTAGTACCA 600
QY 61 TGCCTTACAAGAGAGAAAAGACCGTGCATGCCGATGGTGGAGTACGTTAGTACGA 120

PT such as gene transfer, gene therapy and in DNA immunization.
 XX Claim 18; SEQ ID NO 3; 52pp; English.
 XX The invention relates to multicistronic eukaryotic expression vectors for
 CC the expression of at least two proteins of interest which may be
 CC identical or different. The vectors comprise at least one eukaryotic
 CC expression cassette having a promoter/enhancer sequence, an intron
 CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
 CC and a chain terminator. The vectors may additionally contain a
 CC transcription pause site downstream of the chain terminator. The
 CC invention also encompasses eukaryotic host cells comprising a vector of
 CC the invention, and the recombinant expression of two or more eukaryotic
 CC proteins using host cells transformed with a vector of the invention.
 CC The vectors are useful in various biotechnological applications in which
 CC the simultaneous expression of two or more genes is necessary, such as
 CC gene transfer protocols, DNA immunisation, or for the expression of
 CC different molecules in the same cell. They may also be used in gene
 CC therapy. The present sequence represents a specifically claimed vector
 CC designated PL249, which comprises a cytomegalovirus (CMV)
 CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
 CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous
 CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, and a rabbit
 CC beta-globin gene MRG terminator as well as a kanamycin resistance gene.
 XX
 SQ Sequence 7086 BP; 1870 A; 1699 C; 1753 G; 1764 T; 0 U; 0 Other;
 Query Match 99.4%; Score 262.4; DB 9; Length 7086;
 Best Local Similarity 99.6%; Pred. No. 2.3e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGATGAGTTAGCAACA 60
 Db 1796 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGATGAGTTAGCAACA 1737
 QY 61 TGCTTTACAGAGAGAGAAAAGACACCGTGCATGCGGATTTGGTGGAGTAAGTGTACGA 120
 Db 1736 TGCTTTACAGAGAGAGAAAAGACACCGTGCATGCGGATTTGGTGGAGTAAGTGTACGA 1677
 QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGATGTAAGCAACCACTAAATT 180
 Db 1676 TCGTGCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGATGTAAGCAACCACTAAATT 1617
 QY 181 CCGCATTCGAGAGATATTGATTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGACC 240
 Db 1616 CCGCATTCGAGAGATATTGATTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGACC 1557
 QY 241 ATTCACACATTTGGTGTGCACCTC 264
 Db 1556 ATTCACACATTTGGTGTGCACCTC 1533
 RESULT 10
 AAAS9078
 ID AAAS9078 standard; DNA; 8238 BP.
 XX
 AC AAAS9078;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Nucleotide sequence of a plasmid.
 XX
 KW Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN WO200042208-A1.
 XX
 PD 20-JUL-2000.
 XX
 PF 14-JAN-2000; 2000WO-EP000265.
 XX

PR 14-JAN-1999; 99US-0115920P.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;
 XX Skripchenko Y;
 XX WPI; 2000-476068/41.
 XX
 PT New nucleic acid comprising an adenovirus tripartite leader nucleotide
 PT for producing high-capacity and targeted vectors for adenovirus-based
 PT gene therapy.
 XX
 PS Disclosure; Page 195-198; 212pp; English.
 XX
 CC The specification describes a nucleic acid molecule comprising an
 CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
 CC comprising two different TPL exons or three same or different TPL exons.
 CC The nucleic acid is used to produce an adenovirus vector particle,
 CC deliver an exogenous gene to a target cell, pseudotype recombinant viral
 CC vectors, target an adenovirus vector to a cell, produce a modified
 CC adenovirus, deliver a heterologous gene to an animal and produce a
 CC gutless adenoviral vector particle. The present sequence represents a
 CC plasmid, which is used in the course of the invention
 XX
 SQ Sequence 8238 BP; 1762 A; 2156 C; 2340 G; 1980 T; 0 U; 0 Other;
 Query Match 99.4%; Score 262.4; DB 3; Length 8238;
 Best Local Similarity 99.6%; Pred. No. 2.5e-81;
 Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AATCTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGATGAGTTAGCAACA 60
 Db 541 AATCTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTAACGATGAGTTAGCAACA 600
 QY 61 TGCCTTACAGAGAGAGAAAAGACACCGTGCATGCGGATTTGGTGGAGTAAGTGTACGA 120
 Db 601 TGCCTTACAGAGAGAGAAAAGACACCGTGCATGCGGATTTGGTGGAGTAAGTGTACGA 660
 QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGATGTAAGCAACCACTAAATT 180
 Db 661 TCGTGCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGATGTAAGCAACCACTAAATT 720
 QY 181 CCGCATTCGAGAGATATTGATTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGACC 240
 Db 721 CCGCATTCGAGAGATATTGATTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGACC 780
 QY 241 ATTCACACATTTGGTGTGCACCTC 264
 Db 781 ATTCACACATTTGGTGTGCACCTC 804
 RESULT 11
 AAL56867
 ID AAL56867 standard; DNA; 33622 BP.
 XX
 AC AAL56867;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE DNA sequence of the recombinant adenoviral Av3nBg vector.
 XX
 KW Fibre shaft modification; adenoviral vector; cell entry pathway; penton;
 KW CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;
 KW gene therapy; fibre knob; Av3nBg; ds.
 XX
 OS Human adenovirus type 5.
 OS Unidentified.
 XX
 PN WO20003062400-A2.
 XX

Db 721 CCGCATGAGAGATATTGATTAGTGCCTAGTCGATCAATTAACGCCATTGACC 780

Qy 241 ATTACACACATGTTGGTGCACCTC 264

Db 781 ATTACACACATGTTGGTGCACCTC 804

RESULT 13

AAU56866

ID AAU56866 standard; DNA; 35211 BP.

AC AAU56866;

DT 06-NOV-2003 (first entry)

XX DNA sequence of the recombinant adenoviral AvinBg vector.

XX Fibre shaft modification; adenoviral vector; cell entry pathway; penton;

KW CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;

KW gene therapy; fibre knob; AvinBg; ds.

XX Human adenovirus type 5.

OS Unidentified.

XX WO2003062400-A2.

XX 31-JUL-2003.

XX 24-JAN-2003; 2003WO-US002295.

XX 24-JAN-2002; 2002US-0350388P.

XX 26-JUN-2002; 2002US-0391967P.

XX (SRI) SCRIPPS RBS INST.

PA (NOVS) NOVARTIS AG.

XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;

XX WPI; 2003-627459/59.

XX New modified adenovirus capsid protein, useful as a base vector for

PT producing redirected adenoviruses.

XX Example 1; Page 146-156; 132pp; English.

XX This invention relates to novel fibre shaft modifications in adenoviral

CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a

CC specific targeted tissue or organ, accordingly gene therapy requires the

CC ablation of normal virus tropism. If successful, systemic vector delivery

CC into a peripheral vein would be targeted to the desired location in the

CC body without any associated side effects, which would permit lower, less

CC toxic vector doses that are also potentially less immunogenic. The

CC present invention describes capsid modifications, specifically fibre

CC shaft mutations that when expressed on adenoviral particles ablates

CC binding to heparin sulphate proteoglycans (HSP) thus providing targeted

CC vectors. Furthermore, when this is combined with modifications of other

CC adenoviral proteins involved in the cell entry pathway such as the fibre

CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors

CC become fully targeted. As such, these fully ablated particles can be

CC used in vivo as base vectors for producing redirected adenoviruses with

CC the desired cell specificity. This polynucleotide sequence is the

CC recombinant E1 and E3-deleted adenoviral vector (AvinBg) that encodes a

CC nuclear localising beta-galactosidase, used in the exemplification of the

CC invention

XX

SQ Sequence 35211 BP; 8136 A; 10028 C; 9704 G; 7343 T; 0 U; 0 Other;

Query Match 99.4%; Score 262.4; DB 8; Length 35211;

Best Local Similarity 99.6%; Pred. No. 4.7e-81;

Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTGATGAGTTAGCAACA 60

Db 647 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTGATGAGTTAGCAACA 706

Qy 61 TGCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 120

Db 707 TGCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAGTAAGTGGTACGA 766

Qy 121 TCGTGGCTTATTAGNAGGCAACAGACGGGTCTGACATGGATTGGACCAACCACTAAAT 180

Db 767 TCGTGGCTTATTAGNAGGCAACAGACGGGTCTGACATGGATTGGACCAACCACTAAAT 826

Qy 181 CCGCATTCAGAGATATTGATTAAAGTGCCTAGTCGATCAATTAAGCCATTGACC 240

Db 827 CCGCATTCAGAGATATTGATTAAAGTGCCTAGTCGATCAATTAAGCCATTGACC 886

Qy 241 ATTACACACATGTTGGTGCACCTC 264

Db 887 ATTACACACATGTTGGTGCACCTC 910

RESULT 14

AAZ29699

ID AAZ29699 standard; DNA; 11627 BP.

XX AAZ29699;

DT 22-MAR-2000 (first entry)

XX Viral expression vector, RCASBP(A) construct.

XX Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;

KW viral expression vector; RCASBP(A) construct; replication competent;

KW Bryan polymerase; BP; 'A' type envelope glycoprotein; mutant Src;

KW inflammatory disease; arthritis; rheumatoid arthritis; restenosis;

KW diabetic retinopathy; osteoporosis; cancer; ds.

XX Synthetic.

OS Avian sarcoma virus.

XX

XX Key Location/Qualifiers

FT LTR 1..101

FT repeat_unit /tag= a

FT /tag= b

FT /pt type= DIRECT

FT misc_feature 22..101

FT /tag= c

FT /note= "5' end unique sequence"

FT CDS 372..2483

FT /tag= d

FT /product= "gag protein"

FT /note= "proteins of nucleoprotein core of the virion"

FT mat_peptide 372..902

FT /tag= e

FT /label= gag p19_peptide

FT misc_recomb 388..391

FT /tag= f

FT /note= "Splice donor site"

FT mat_peptide 909..1094

FT /tag= g

FT /label= gag p10_peptide

FT mat_peptide 1095..1814

FT /tag= h

FT /label= gag p27_peptide

FT mat_peptide 1843..2108

FT /tag= i

FT /label= gag p12_peptide

FT mat_peptide 2109..2480

FT /tag= j

FT /label= gag p15_peptide

FT CDS 2501..5189

FT /tag= k

FT /product= "Reverse transcriptase polymerase (pol)"

```
FT mat_peptide 2501..4216
FT /tag= 1
FT /label= Polymerase_pol_pt
FT 4217..5186
FT /tag= m
FT /label= Polymerase_pol_in
FT 5075..5078
FT /tag= n
FT /note= "env splice acceptor site"
FT 5245..6882
FT /tag= o
FT /product= "Envelope protein (env)"
FT 5245..6264
FT /tag= p
FT /label= env_gp85_peptide
FT 6265..6879
FT /tag= q
FT /label= env_gp37_peptide
FT 6983..6986
FT /tag= r
FT /note= "Clal splice acceptor site"
FT 7154..7165
FT /tag= s
FT /label= PPT
FT 7166..7494
FT /tag= t
FT 7166..7394
FT /tag= u
FT /note= "3'end unique sequence"
FT 7395..7415
FT /tag= v
FT /rpt_type= DIRECT
FT 7416..7494
FT /tag= w
FT /note= "5'end unique sequence"
FT 7649..11258
FT /tag= x
FT /label= pBR322_vector
FT 11394..11623
FT /tag= y
FT /note= "3'end unique sequence"
XX
XX WO9961590-A1.
XX
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011780.
XX
XX 29-MAY-1998; 98US-0087220P.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Cheresch DA, Eliceiri B, Schwartzberg PL;
XX
XX WPI; 2000-116335/10.
XX
XX Using tyrosine kinase Src for modulating angiogenesis in tissues useful
XX in, e.g. treatment of chronic articular rheumatism.
XX
XX Claim 15; Page 59-66; 80pp; English.
XX
XX The present DNA sequence is the viral expression vector, RCASBP(A)
XX construct. This vector is based on a replication competent avian sarcoma
XX virus with an enhanced Bryan polymerase (BP) and is specific for the 'A'
XX type envelope glycoprotein expressed on normal avian cells. The vector
XX expresses Src protein or modified Src, that can be used to modulate
XX angiogenesis. When the Src protein is inactivated, angiogenesis is
XX inhibited, while when it is activated, angiogenesis is potentiated. This
XX modified or mutant Src can be used to treat inflammatory diseases like,
XX arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis,
XX osteoporosis and cancer associated disorders
XX
XX Sequence 11627 BP; 2796 A; 2808 C; 3324 G; 2699 T; 0 U; 0 Other;
```

```
Query Match 99.0%; Score 261.4; DB 3; Length 11627;
Best Local Similarity 99.6%; Pred. No. 6.5e-81;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 60
Db 7166 AATGTAGTCTTATGCAATCTCTTGTAGTCTTTGCAACATGTAACGATGAGTTAGCAACA 7225

Qy 61 TGCCTTACAGGAGAGAAAAGCAGCCGTCATGCGGATTTGTTGGAGTAAGTGGTACGA 120
Db 7226 TGCCTTACAGGAGAGAAAAGCAGCCGTCATGCGGATTTGTTGGAGTAAGTGGTACGA 7285

Qy 121 TCGTGCCTTATTAGGAGGCAACAGACGCGGTCTGACATGATTTGACGAAACCACTAAATT 180
Db 7286 TCGTGCCTTATTAGGAGGCAACAGACGCGGTCTGACATGATTTGACGAAACCACTAAATT 7345

Qy 181 CCGCATTCGAGAGATATTGATTAAAGTGCCTAGCTCGATACATATAACGCCATTGACC 240
Db 7346 CCGCATTCGAGAGATATTGATTAAAGTGCCTAGCTCGATACATATAACGCCATTGACC 7405

Qy 241 ATTCACACATTTGTTGCACCT 263
Db 7406 ATTCACACATTTGTTGCACCT 7428

RESULT 15
ABZ23249
ID ABZ23249 standard; DNA; 2245 BP.
XX
XX AC ABZ23249;
XX
XX 24-MAR-2003 (first entry)
XX
XX Lac repressor operated p21-expression cassette and RSV-LTR promoter.
XX
XX Lac repressor; p21; RSV; LTR promoter; cell cycle inhibitor protein;
XX protein production; anchorage-independent producer cell line; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX promoter 1..563
XX /tag= a
XX /note= "RSV-LTR promoter"
XX intron 564..1051
XX /tag= b
XX /note= "SV40 small t antigen intron"
XX misc_feature 1052..1907
XX /tag= c
XX /note= "p21 coding sequence"
XX polyA_signal 1908..2245
XX /tag= d
XX /note= "thymidine kinase polyA site"
XX
XX WO000299100-A2.
XX
XX 12-DEC-2002.
XX
XX 03-JUN-2002; 2002WO-EP006054.
XX
XX 01-JUN-2001; 2001GB-00013318.
XX
XX (LONZ ) LONZA BIOLOGICS PLC.
XX
XX Al-Rubeai M, Shuttleworth J;
XX
XX WPI; 2003-148669/4.
XX
XX Producing recombinant protein, particularly for maximizing or enhancing
XX e.g. therapeutic protein production, by co-expressing protein with
XX recombinant cell cycle inhibitor protein (p21) in producer cell line.
XX
```


OS Human respiratory syncytial virus.
 PN WO200170816-A2.
 XX
 XX
 PD 27-SEP-2001.
 XX
 XX 21-MAR-2001; 2001WO-US009050.
 XX
 XX 22-MAR-2001; 2000US-0191355P.
 PR
 PR 20-FEB-2001; 2001US-0269799P.
 XX
 XX (ROHM) ROHM & HAAS CO.
 PA
 XX
 XX Palli SR, Kapitskaya MZ, Cress DE;
 XX
 XX WPI; 2001-656841/75.
 DR
 XX
 XX Bcdysone and retinoid X receptor based inducible gene expression systems
 FT for use in e.g. gene therapy, large scale production of proteins and cell
 FT -based high-throughput screening assays.
 PT
 XX
 XX Example 1; Page 141; 144pp; English.
 PS
 XX The invention relates to Bcdysone and retinoid X receptor based inducible
 CC gene expression systems useful for modulating gene expression in host
 CC cells. The gene expression system encodes a polypeptide with a DNA-
 CC binding domain recognizes a response element associated with a gene whose
 CC expression is to be modulated and/or a ligand binding domain (LBD)
 CC comprising a LBD from a nuclear receptor and a second gene expression
 CC cassette capable of being expressed in a host cell comprising a
 CC polynucleotide sequence encoding a second polypeptide comprising a trans-
 CC activation domain and/or a LBD comprising a LBD from a nuclear receptor
 CC other than ultraspriacle (USP) (the trans-activation domain is from a
 CC nuclear receptor other than an ecdysone receptor, a retinoid X receptor
 CC or a USP receptor and the LBDs from the first and second polypeptides are
 CC different and dimerise). The ecdysone and retinoid X receptor based
 CC inducible gene expression systems useful for modulating gene expression
 CC in host cells, for use in gene therapy, large scale production of
 CC proteins and antibodies, cell-based high-throughput screening assays
 CC (HTS), functional genomic and regulation of traits in transgenic plants
 CC and animals. The present sequence represents promoter from human
 CC respiratory syncytial virus (RSV) which is used in an inducible gene
 CC expression system of the invention
 XX
 SQ Sequence 262 BP; 79 A; 53 C; 64 G; 66 T; 0 U; 0 Other;

Query Match 97.4%; Score 257.2; DB 4; Length 262;
 Best Local Similarity 98.9%; Pred. No. 3.7e-80;
 Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACAT 61
 DB 1 ATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACAT 60
 QY 62 GCCTTCAAGGAGAGAAAAGACCCGTCGATGCCGATGCTTGAAGTGAAGTGGTACGAT 121
 DB 61 GCCTTCAAGGAGAGAAAAGACCCGTCGATGCCGATGCTTGAAGTGAAGTGGTACGAT 120
 QY 122 CGTGCCTTATAGGAGGACACAGACGGGCTCTGCATGATTCGACGATTCGACCACTTAATTC 181
 DB 121 CGTGCCTTATAGGAGGACACAGACGGGCTCTGCATGATTCGACGATTCGACCACTTAATTC 180
 QY 182 CGCATTCGAGAGATTTGATTTAAGTGCCTAGCTCGATACATTAAGCCATTTGACCA 241
 DB 181 CGCATTCGAGAGATTTGATTTAAGTGCCTAGCTCGATACATTAAGCCATTTGACCA 240
 QY 242 TTCACCACTTGGTGGACCT 263
 DB 241 TTCACCACTTGGTGGACCT 262

RESULT 19
 ABZ23250

ABZ23250 standard; DNA; 562 BP.
 XX
 XX ABZ23250;
 XX
 XX 24-MAR-2003 (first entry)
 DT
 XX
 XX Nucleotide sequence of the Rous sarcoma virus (RSV)-LTR promoter.
 DE
 XX p21; RSV; LTR promoter; cell cycle inhibitor protein; protein production;
 KW anchorage-independent producer cell line; ss.
 XX
 XX Rous sarcoma virus.
 OS
 XX WO200299100-A2.
 PN
 XX 12-DEC-2002.
 PD
 XX 03-JUN-2002; 2002WO-BP06054.
 PF
 XX 01-JUN-2001; 2001GB-00013318.
 PR
 XX (LONZ) LONZA BIOLOGICS PLC.
 PA
 XX Al-Rubeai M, Shuttleworth J;
 FI
 XX WPI; 2003-148669/14.
 DR
 XX Producing recombinant protein, particularly for maximizing or enhancing
 PT e.g. therapeutic protein production, by co-expressing protein with
 PT recombinant cell cycle inhibitor protein (p21) in producer cell line.
 FT
 XX Disclosure; Page 32-33; 33pp; English.
 PS
 XX The present sequence represents the Rous sarcoma virus (RSV)-LTR
 CC promoter. The present sequence is used to produce vectors for use in the
 CC method of the invention. The specification describes a method for
 CC producing a protein, preferably a recombinant protein, in a mammalian
 CC anchorage-independent producer cell line. The method comprises co-
 CC expressing with the protein in the producer cell line a recombinant cell
 CC cycle inhibitor protein (preferably p21). The method is useful for
 CC producing a recombinant protein in a producer cell line. This is
 CC particularly useful for maximizing or enhancing the production of e.g.
 CC therapeutic proteins at an industrial scale
 XX
 SQ Sequence 562 BP; 143 A; 109 C; 163 G; 147 T; 0 U; 0 Other;

Query Match 97.1%; Score 256.4; DB 7; Length 562;
 Best Local Similarity 99.6%; Pred. No. 1e-79;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 60
 DB 305 AATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGCTTAACGATGAGTTAGCAACA 364
 QY 61 TGCCTTCAAGGAGAGAAAAGACCCGTCGATGCCGATGCTTGAAGTGAAGTGGTACGAT 120
 DB 365 TGCCTTCAAGGAGAGAAAAGACCCGTCGATGCCGATGCTTGAAGTGAAGTGGTACGAT 424
 QY 121 TCGTGCCTTATAGGAGGACACAGACGGGCTCTGCATGATTCGACGATTCGACCACTTAATTC 180
 DB 425 TCGTGCCTTATAGGAGGACACAGACGGGCTCTGCATGATTCGACGATTCGACCACTTAATTC 484
 QY 181 CGCATTCGAGAGATTTGATTTAAGTGCCTAGCTCGATACATTAAGCCATTTGACCA 240
 DB 485 CGCATTCGAGAGATTTGATTTAAGTGCCTAGCTCGATACATTAAGCCATTTGACCA 544
 QY 241 ATTCACCACTTGGTGGTGC 258
 DB 545 ATTCACCACTTGGTGGTGC 562

RESULT 20
 ADD35599

proteins using host cells transformed with a vector of the invention. The vectors are useful in various biotechnological applications in which the simultaneous expression of two or more genes is necessary, such as gene transfer protocols, DNA immunisation, or for the expression of different molecules in the same cell. They may also be used in gene therapy. The present sequence represents a specifically claimed vector designated pL250, which comprises a cytomegalovirus (CMV) promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV) IRGS, an SV40 polyadenylation site, a transcription pause site, a Kous sarcoma virus (RSV) promoter, rabbit beta-globin intron, the hepatitis C virus (HCV) IRES, and a rabbit beta-globin gene mRSG terminator as well as a kanamycin resistance gene.

RESULT 22	
AAZ94161	
ID	AAZ94161 standard; DNA; 397 BP.
XX	XX
AC	AAZ94161;
XX	XX
DT	19-JUN-2000 (first entry)
DE	395 Nucleic acid Rous sarcoma virus promoter.
XX	XX
KW	Adenovirus; vector; RSV; promoter; prostate cancer; gene therapy;
KW	tumour suppressor gene; p16; ss.
XX	XX
OS	Rous sarcoma virus.
XX	XX
WO	WO200014211-A1.
XX	XX
PD	16-MAR-2000.
XX	XX
PF	02-SEP-1999; 99WO-US018833.
XX	XX
PR	02-SEP-1998; 98US-00145729.
XX	XX
PA	(GENO-) GENOTHERAPEUTICS INC.
XX	XX
PI	Steiner MS, Lu Y;
XX	XX
DR	WPI; 2000-256967/22.
XX	XX
PT	Replication-deficient adenovirus type 5 expression vector, useful in gene
PT	therapy of prostate cancer, comprises a nucleic acid encoding p16 under
PT	the control of a Rous Sarcoma virus promoter.
XX	XX

BS Claim 1; Page 12; 118pp; English.

XX CC The present sequence is that of 395 nucleic acid Rous sarcoma virus (RSV) promoter. A novel replication-deficient adenovirus type 5 expression vector of the invention, termed AdRSVP16 (see AAZ94163), has a deletion in an E1 and E3 region of the genome and contains a p16 tumour suppressor gene under the control of the RSV promoter. The adenoviral vector is used in the gene therapy of prostate cancer, in which p16 is frequently abnormal. Gene therapy is used to replace a missing, mutated or inactivated p16 tumour suppressor gene, thereby inhibiting the growth and/or progression of the tumour

XX CC
SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 3; Length 397;
Best Local Similarity 98.5%; Pred. No. 6.6e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCCTATTGCAATACTCTTTGAGTCTTTGCCAATCGTAACGATGACTTAGCAACA 60
Db 132 AATGTAGTCCTATTGCAATACTCTTTGAGTCTTTGCCAATCGTAACGATGACTTAGCAACA 191
Qy 61 TGCCCTTACAGGAGAGAAAAAGCACCCTGCATGCCGATTCGGTGGAAGTAAGTGTTGATAGA 120
Db 192 TGCCCTTACAGGAGAGAAAAAGCACCCTGCATGCCGATTCGGTGGAAGTAAGTGTTGATAGA 251
Qy 121 TCGTGCCTTTATTAGGAAGGCAACAAGACGGCTCTGCATTCGATTCGACGCAACCACTAAATT 180
Db 252 TCGTGCCTTTATTAGGAAGGCAACAAGACGGCTCTGCATTCGATTCGACGCAACCACTAAATT 311
Qy 181 CGCATTCGACAGAT-ATTGTATTTAAGTCGCTAGCTCGATACATAAATAAGCGCAATTGCAC 239
Db 312 CGCATTCGACAGATAATTGTATTTAAGTCGCTAGCTCGATACATAAATAAGCGCAATTGCAC 371
Qy 240 CATTCACCAACATTGGGTGCACCTC 264
Db 372 CATTCACCAACATTGGGTGCACCTC 396

RESULT 23
AAAL4719
ID AAAL4719 standard; DNA; 397 BP.
XX AC AAAL4719;
XX DT 08-AUG-2000 (first entry)
DE Nucleotide sequence of the Rous Sarcoma virus promoter.
XX Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;
KW replication-deficient adenovirus type 5; suicide gene therapy;
KW cancer cell; chemotherapy; beta-lactamase prodng enzyme; prodrug TCM;
KW anticancer; tumor; leukemia; breast cancer; Wilms' tumor;
KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;
KW papillary adenocarcinoma; promoter; ss.
OS Rous sarcoma virus.
WP WO200020608-A1.
PN WO200020608-A1.
PD 13-APR-2000.
XX 01-OCT-1999; 99WO-US020908.
XX 02-OCT-1998; 98US-00165321.
PA (GENO-) GENOTHERAPEUTICS INC.
FI Steiner MS;
XX WPI; 2000-303788/26.
XT Treating cancer using viral vectors which encode enzymes that convert

PT inactive drugs to active cytotoxic agents, expression of the enzyme is
PT tissue specific therefore targeting the effects of the drug to tumor
XX cells.
PS Disclosure; Page 13-14; 130pp; English.
XX The specification describes a method for inducing cellular cytotoxicity
CC in tumor cells using replication-deficient adenovirus type 5 expression
CC vectors. The vectors comprise a sequence encoding a beta-lactamase under
CC the control of a Rous Sarcoma virus in combination with a prodrug
CC conjugated to a toxic agent. Tissue specific expression of the enzyme
CC converts the inactive drugs into active cancer killing agents. The
CC adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-
CC lactamase sequence is inserted within this region. The vectors are used
CC for suicide gene therapy. This involves introducing genes into cancer
CC cells that encode enzymes capable of converting inactive drugs into
CC active cancer killing agents. If tissue specific promoters are coupled to
CC the prodrug enzymes, then production of the prodrug will be tissue
CC specific and targeted to the tumor. Therefore the cancer cells act as
CC their own factories to activate chemotherapy agents and commit suicide.
CC Beta-lactamase prodrug enzymes convert prodrug TCM into an active
CC anticancer agent which is cytotoxic to cancer cells pEC-1. The method is
CC used to treat patients with cancers of the brain, bladder or prostate. It
CC may also be used to treat a range of other tumors such as leukemia,
CC breast cancer, Wilms tumor, small cell lung carcinoma, Ewing's sarcoma,
CC colon carcinoma and papillary adenocarcinomas. The present sequence
CC represents the the Rous Sarcoma virus promoter, which was used to
CC construct vectors of the invention
XX

SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 3; Length 397;
Best Local Similarity 98.5%; Pred. No. 6.6e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAATGCTTAACGATGAGTACCA 60
DB 132 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAATGCTTAACGATGAGTACCA 191
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGCTGGAAGTGGTACCA 120
DB 192 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGCTGGAAGTGGTACCA 251
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGCGGTCTGCATGATGATGGAACCACTAAATT 180
DB 252 TCGTGCCTTATTAGGAGGCAACAGACGCGGTCTGCATGATGATGGAACCACTAAATT 311
QY 181 CCGCATTCGAGAGAT-ATTGTATTATTAGTGCCTAGCTGCATACATATAACGCCATTGAC 239
DB 312 CCGCATTCGAGAGATATTGTATTATTAGTGCCTAGCTGCATACATATAACGCCATTGAC 371
QY 240 CATTACCACTATTGGTGTGCACCTC 264
DB 372 CATTACCACTATTGGTGTGCACCTC 396

RESULT 24
AAZ93077
ID AAZ93077 standard; DNA; 397 BP.
XX
XX AAZ93077;
AC
XX
XX 04-JUL-2000 (first entry)
DT
XX
XX Rous Sarcoma Virus promoter sequence.

XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
XX Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
XX prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
XX
XX Rous sarcoma virus.
XX
XX
XX WC200014256-A1.

XX 16-MAR-2000.
XX 03-SEP-1999; 99WO-US018834.
XX 04-SEP-1998; 98US-00148275.
XX (GENO-) GENOTHERAPEUTICS INC.
XX Steiner MS, Lu Y;
XX WPI; 2000-257001/22.
XX Replication-deficient adenovirus type 5 expression vectors used for gene
PT therapy of cancer, especially prostate cancer, comprising an insertion of
PT nucleic acid encoding cytochrome p450 genes.
XX
XX Claim 8; Page 18; 110pp; English.
XX Replication-deficient adenovirus type 5 expression vectors comprise an
CC adenovirus genome with a deletion in the E1 and E2 region of the genome
CC and an insertion within the region under the control of a Rous Sarcoma
CC Virus promoter can be used to induce chemotoxicity in tumour cells. Three
CC such expression vectors are described, the inserted nucleic acids in each
CC being the following: Vector (I) has an insertion of a nucleic acid
CC encoding a cytochrome 2C9 p450 and is designated AdRSV2C9 (ATCC VR-
CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
CC cytochrome 3A4 p450 and is designated AdRSV3A4 (ATCC VR-2629). Vector
CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
CC designated AdRSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
CC can be induced by administering (I) and (III) or (II) and (III) into the
CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell
CC to a prodrug and then administering the prodrug which kills the cell,
CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
CC therapy to transfer a drug susceptibility gene to the tumor which
CC activates a nontoxic prodrug intratumorally so the released drug can kill
CC the tumor cells containing the drug susceptibility gene
XX

SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 3; Length 397;
Best Local Similarity 98.5%; Pred. No. 6.6e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAATGCTTAACGATGAGTACCA 60
DB 132 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAATGCTTAACGATGAGTACCA 191
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGCTGGAAGTGGTACCA 120
DB 192 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGCTGGAAGTGGTACCA 251
QY 121 TCGTGCCTTATTAGGAGGCAACAGACGCGGTCTGCATGATGATGGAACCACTAAATT 180
DB 252 TCGTGCCTTATTAGGAGGCAACAGACGCGGTCTGCATGATGATGGAACCACTAAATT 311
QY 181 CCGCATTCGAGAGAT-ATTGTATTATTAGTGCCTAGCTGCATACATATAACGCCATTGAC 239
DB 312 CCGCATTCGAGAGATATTGTATTATTAGTGCCTAGCTGCATACATATAACGCCATTGAC 371
QY 240 CATTACCACTATTGGTGTGCACCTC 264
DB 372 CATTACCACTATTGGTGTGCACCTC 396

RESULT 25
AAQ75974/c
ID AAQ75974 standard; cDNA; 4059 BP.
XX
XX AAQ75974;
AC
XX
XX 25-MAR-2003 (revised)
DT

23-AUG-1995 (first entry)
 pHLA-B7 expression vector.
 expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
 light beta-2 microglobulin; class I major histocompatibility complex;
 MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
 Synthetic.
 Key Location/Qualifiers
 misc_feature 1..354
 /note= "PBR322 backbone contg. bacterial origin of replication"
 355..1170
 /tag= b
 /note= "Kanamycin resistance gene open reading frame; the gene is taken from the transposable element Tn903"
 complement(1410..1177)
 /tag= c
 /note= "SV40 polyA signal sequence"
 complement(1412..1560)
 /tag= d
 /note= "SV40 small t intron"
 complement(1561..1794)
 /tag= e
 /note= "3' untranslated region of HLA-B7 heavy chain mRNA"
 complement(1795..2880)
 /tag= f
 /note= "HLA-B7 open reading frame"
 complement(2886..3415)
 /tag= g
 /note= "Rous sarcoma virus 3' LTR promoter region"
 3416..4059
 /tag= h
 /note= "PBR322 backbone"
 WO9429469-A2.
 22-DEC-1994.
 27-MAY-1994; 94WO-US006069.
 07-JUN-1993; 93US-00074344.
 (VICIA-) VICAL INC.
 (UNMI) UNIV MICHIGAN.
 Nabel GJ, Nabel EG, Lew D, Marquet M;
 WPI; 1995-036494/05.
 New vectors for gene therapy, partic for tumours - comprising genetic material encoding one or more cistron(s) which express immunogenic or therapeutic peptide(s).
 Claim 9; Page 42-43; 50pp; English.
 This HLA-B7 antigen encoding plasmid was developed to incorporate many advantageous features, eg. the kanamycin resistance gene. The eradication of two open reading frames encoding portions of SV40 viral proteins lowers the risk of tumorigenicity. The vector may also operate as a cassette into which cistrons may be inserted and removed at will for the transcription and subsequent translation of peptides of interest. The vector is used partic. for the treatment of neoplastic disease, eg. melanoma, and provides enhanced gene delivery and expression in vivo.
 (Updated on 25-MAR-2003 to correct PN field.)
 Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T; 0 U; 0 Other;
 Query Match 94.0%; Score 248.2; DB 2; Length 4059;

Best Local Similarity 98.5%; Pred. No. 1.8e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGCTTATGCATATCTCTGTAGTCTTGCACATGTTAAAGATGATTAGCAACA 60
 Db 3156 AATGTAGCTTATGCATATCTCTGTAGTCTTGCACATGTTAAAGATGATTAGCAACA 3097
 QY 61 TGCCTTACAG 120
 Db 3096 TGCCTTACAG 3037
 QY 121 TCGTGCCTTATTAG 180
 Db 3036 TCGTGCCTTATTAG 2977
 QY 181 CCGCATTGCAGAGAT-ATTGTAATTTAAAGTGGCTAGCTCGATACATATAAGCCATTGAC 239
 Db 2976 CCGCATTGCAGAGATATTGTAATTTAAAGTGGCTAGCTCGATACATATAAGCCATTGAC 2917
 QY 240 CATTACACCAATTGGTGTGCACCTC 264
 Db 2916 CATTACACCAATTGGTGTGCACCTC 2892
 RESULT 26
 ID AAQ62391 standard; DNA; 4341 BP.
 AC AAQ62391;
 DT 25-MAR-2003 (revised)
 DT 18-NOV-1994 (first entry)
 XX Vector pVAC1.
 DE Vector; pVAC1; pRc/RSV; leader sequence; termination signal;
 KW fusion protein; pSfi/Not.Tag1; pSfi leader; human; immunoglobulin; VHL;
 KW single chain; Fv; murine antibody; retroviral; envelope; plasmid;
 KW vaccine; ss.
 OS Synthetic.
 XX Key Location/Qualifiers
 PH misc_RNA complement(1..775)
 FT /tag= c
 FT /note= "Claim 9"
 FT misc_RNA 606..780
 FT /tag= b
 FT /note= "Claim 8"
 FT misc_RNA 606..716
 FT /tag= a
 FT /note= "Claim 7"
 XX WO9408008-A1.
 XX 14-APR-1994.
 XX 04-OCT-1993; 93WO-GB002054.
 XX 02-OCT-1992; 92GB-00020808.
 XX (MEDI-) MEDICAL RES COUNCIL.
 XX Hawkins RE, Russell SU, Stevenson FK, Winter GP;
 PI WPI; 1994-135575/16.
 DR Modulating immune response to a disease marker - by administering a
 XX vector which expresses the disease marker to interact with the immune
 PT system.
 XX Claim 10; Fig 7; 77pp; English.
 XX

CC This sequence represents the vector pVAC1. This vector is based on the
 CC commercially available vector pRC/RSV. Leader sequences and termination
 CC signals were introduced into the vector to allow for production of fusion
 CC proteins. The vector, pSfi/Not-Tag1, was modified to replace the pEB
 CC leader with the human immunoglobulin VH1 leader sequence that permits the
 CC encoding of an SfiI cloning site without modification of the amino acid
 CC sequence. This fragment was then cloned as an EcoRI/Blunt-HindIII
 CC fragment into NotI/Blunt- HindIII cut vector pRC/RSV to give pVAC1. The
 CC single chain Fv for an individual patient can be inserted within the VH1
 CC leader sequence. This plasmid when encoding a single chain murine
 CC antibody/retroviral fusion protein can be used as a plasmid
 CC vaccine and it induces a strong humoral response to the antibody moiety
 CC in BAUB/c mice. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 4341 BP; 1032 A; 1099 C; 1091 G; 1119 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 2; Length 4341;
 Best Local Similarity 98.5%; Pred. No. 1.9e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAAACGATGAGTTAGCAACA 60
 DB 340 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAAACGATGAGTTAGCAACA 399
 QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTTGGTGAAGTAAGTGTACGA 120
 DB 400 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTTGGTGAAGTAAGTGTACGA 459
 QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGTTGGAAGCAACCACTAAATT 180
 DB 460 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGTTGGAAGCAACCACTAAATT 519
 QY 181 CGCGATTGACAGAGAT-ATTGTATTATTAGTGCCTAGCTCGATACATAAATACCCATTGAC 239
 DB 520 CGCGATTGACAGAGATATTGTATTATTAGTGCCTAGCTCGATACATAAATACCCATTGAC 579
 QY 240 CATTACACCACATTGGTGTGCACCTC 264
 DB 580 CATTACACCACATTGGTGTGCACCTC 604

RESULT 27
 AAS17704
 ID AAS17704 standard; DNA; 4341 BP.

XX AAS17704;
 AC AAS17704;
 DT 12-MAR-2002 (first entry)
 DE Vector pVAC1 encoding a DNA vaccine.

XX Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTD; PCR primer; pVAC1;
 KW ds.

XX Clostridium tetani.
 OS Homo sapiens.
 CS Synthetic.
 CS Cauliflower mosaic virus.

XX W0200179510-Al.

XX 25-OCT-2001.

XX 17-APR-2001; 2001WO-GB001719.

XX 17-APR-2000; 2000GB-00009470.

XX (CANC-) CANCER RES VENTURES LTD.

XX Rice J, Stevenson F;

XX WPI; 2002-066370/09.

XX

PT Nucleic acid construct, useful to immunize against various diseases
 PT including cancer, express the first domain of tetanus toxin FrC fused
 PT to a disease peptide antigen to provide a vaccine.

XX Disclosure; Fig 4; 71pp; English.

XX The invention relates to a nucleic acid construct for delivery into
 CC living cells in vivo, to induce an immune response to a disease peptide
 CC antigen, where the construct directs expression of a fusion protein
 CC comprising the peptide antigen and the first domain of FrC. Also included
 CC are a nucleic acid vector comprising the above construct, a host cell
 CC comprising the above construct or vector and a method of producing a
 CC nucleic acid construct for inducing an immune response. The method
 CC comprises identifying a nucleic acid sequence encoding a disease peptide
 CC antigen comprising epitopes characteristic of the disease, cloning the
 CC nucleic acid sequence, introducing the cloned nucleic acid into a vector
 CC which allows the antigen to be expressed as a fusion with a first domain
 CC FrC from tetanus toxin, and optionally isolating the construct from the
 CC vector. The construct or vector is used as a vaccine to induce an immune
 CC response, particularly to tumour antigens. The present sequence is vector
 CC pVAC1 which encodes a vaccine of the invention

XX Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 6; Length 4341;
 Best Local Similarity 98.5%; Pred. No. 1.9e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAAACGATGAGTTAGCAACA 60
 DB 340 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAAACGATGAGTTAGCAACA 399
 QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTTGGTGAAGTAAGTGTACGA 120
 DB 400 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTTGGTGAAGTAAGTGTACGA 459
 QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGTTGGAAGCAACCACTAAATT 180
 DB 460 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGTTGGAAGCAACCACTAAATT 519
 QY 181 CGCGATTGACAGAGAT-ATTGTATTATTAGTGCCTAGCTCGATACATAAATACCCATTGAC 239
 DB 520 CGCGATTGACAGAGATATTGTATTATTAGTGCCTAGCTCGATACATAAATACCCATTGAC 579
 QY 240 CATTACACCACATTGGTGTGCACCTC 264
 DB 580 CATTACACCACATTGGTGTGCACCTC 604

RESULT 28

AEN83143
 ID AEN83143 standard; DNA; 4341 BP.

XX AEN83143;

XX 10-SEP-2002 (first entry)

DE Plasmid pVAC1 complete sequence.

KW Immune response; plant viral coat protein; pVAC1; cytostatic; virucide;
 KW cancer; B cell malignancy; ds.

XX Synthetic.

XX W0200240513-A2.

XX 23-MAY-2002.

XX 20-NOV-2001; 2001WO-GB005142.

XX 20-NOV-2000; 2000GB-00028319.

XX (CANC-) CANCER RES VENTURES LTD.

PA

XX Savel'yeva N, Stevenson F;
 XX WPI; 2002-500202/53.
 XX Nucleic acid construct for delivery into living cells as a vaccine,
 XX useful for treating e.g. cancer, directs the expression of a fusion
 XX protein comprising an antigen and an adjuvant sequence derived from a
 XX plant viral coat protein.
 XX Example 3; Fig 7; 84pp; English.
 XX The invention relates to a novel nucleic acid construct for inducing an
 XX immune response in vivo to an antigen, capable of directing the
 XX expression of a fusion protein that comprises an antigen and an adjuvant
 XX sequence derived from a plant viral coat protein. The construct of the
 XX invention has cytostatic and virucide activity. The nucleic acid
 XX construct is useful for inducing an immune response in a patient, for
 XX vaccinating a patient against an infectious disease caused by an antigen
 XX derived from a pathogen e.g. a virus, for treating a cancer patient or a
 XX patient with a predisposition to cancer and for treating a patient having
 XX a B cell malignancy, where the construct is encapsidated, and optionally,
 XX a second nucleic acid sequence encoding a further immunomodulatory
 XX polypeptide is administered to the patient. The construct is also useful
 XX in medical treatment, and in the preparation of a vaccine for treating or
 XX preventing a disease state associated with the antigen. The sequence
 XX shows the complete sequence of vector pVAC1
 XX Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
 XX Query Match 94.0%; Score 248.2; DB 6; Length 4341;
 XX Best Local Similarity 98.5%; Pred. No. 1.9e-76;
 XX Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGCTAGCTTATGCAATCTCTTGTAGTCTTGCACATGTAACGATGATAGCAACA 60
 Db 340 AATGTAGCTTATGCAATCTCTTGTAGTCTTGCACATGTAACGATGATAGCAACA 399
 QY 61 TGCTTACAG 120
 Db 400 TGCTTACAG 459
 QY 121 TGTGCTTATGAG 180
 Db 450 TGTGCTTATGAG 519
 QY 131 CCGCATTTGAGAGAT-ATTGCTATTTAGTCTGCTAGCTGATACATTAACGATTTGAC 239
 Db 520 CCGCATTTGAGAGATTTGCTATTTAGTCTGCTAGCTGATACATTAACGATTTGAC 579
 QY 240 CATTACACCATTTGCTGACCTC 264
 Db 580 CATTACACCATTTGCTGACCTC 604
 RESULT 29
 ID AAT02998
 XX AAT02998 standard; DNA; 5653 BP.
 XX AC AAT02998;
 XX 24-MAR-1996 (first entry)
 XX RSV tar Rev M10 expression plasmid prSVt:RevM10.
 XX Plasmid prSVt:RevM10; particle-mediated gene transfer; cyclic;
 XX Particle acceleration; HIV virus infection; gene therapy; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX misc_feature 1..36
 XX /*tag= a

FT enhancer /note= "pBR322 vector sequence"
 FT 37..610
 FT /*tag= b
 FT /note= "RSV enhancer"
 FT 611..699
 FT /*tag= c
 FT /label= tar
 FT /note= "HIV promoter tat responsive element"
 FT 700..1129
 FT /*tag= d
 FT /note= "Rev M10 open reading frame"
 FT 1243
 FT /*tag= e
 FT /note= "cattle somatotropin poly(A) site"
 FT 1993..2300
 FT /*tag= f
 FT /note= "pSVneo promoter"
 FT 2346
 FT /*tag= g
 FT /label= kanamycin resistance gene
 FT /note= "pSV2 neo Selectable marker gene"
 FT 3360
 FT /*tag= h
 FT /note= "pSV2 neo"
 FT 3459..5653
 FT /*tag= i
 FT /note= "plasmid pUC ori/amp sequence"
 FT XX
 PN W09529703-A1.
 XX 09-NOV-1995.
 XX 01-MAY-1995; 95WO-US005024.
 XX 29-APR-1994; 94US-00235277.
 XX (NABE/) NABEL G J.
 XX (WOFF/) WOFFENDIN C.
 XX (YANG/) YANG N.
 XX (SHEE/) SHEEHY M J.
 XX Nabel GU, Woffendin C, Yang N, Sheehy MJ;
 XX WPI; 1995-403807/51.
 XX Particle-mediated gene transfer - in T cells, monocytes, macrophage(s),
 XX dendrites or haematopoietic stem cells, partic. for treating HIV
 XX infection.
 XX Disclosure; Fig 11a-11e; 96pp; English.
 XX Expression plasmid prSVt:RevM10 contains the Rev M10 HIV protective gene
 XX (a dominant-negative inhibition gene) under the control of the Tar
 XX sequence (HIV promoter -18 to -72), i.e. gene expression is activated by
 XX Tat. The plasmid also contains the kanamycin- resistance selectable
 XX marker gene. The plasmid is used in a particle-mediated gene transfer
 XX process for Rev M10 gene expression in T-cells (preferably), monocytes,
 XX macrophages, haematopoietic stem cells or dendrites. The gold
 XX microparticle acceleration process results in stable incorporation of
 XX foreign genes in the cells. This method is used to treat HIV infection.
 XX Rev M10 transduced cells are resistant to HIV challenge. The method may
 XX be applied to the transfer of other therapeutic genes in a gene therapy
 XX process
 XX Sequence 5653 BP; 1328 A; 1428 C; 1478 G; 1419 T; 0 U; 0 Other;
 XX Query Match 94.0%; Score 248.2; DB 2; Length 5653;
 XX Best Local Similarity 98.5%; Pred. No. 2.1e-76;
 XX Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGCTAGCTTATGCAATCTCTTGTAGTCTTGCACATGTAACGATGATAGCAACA 60
 Db 340 AATGTAGCTTATGCAATCTCTTGTAGTCTTGCACATGTAACGATGATAGCAACA 399

CC activity of the tat protein. The TAR sequence is linked to the protective
 CC gene, and therefore controls its expression. This sequence is a preferred
 CC recombinant nucleic acid vector, designated RSV tar Rev M10 plasmid
 XX
 SQ Sequence 5653 BP; 1326 A; 1429 C; 1478 G; 1420 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 2; Length 5653;
 Best Local Similarity 98.5%; Pred. No. 2.1e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACATCTTGTAGTCTTGTGCAATGTAACGATGAGTTAGCAACA 60
 DB 340 AATGTAGTCTTATGCAATACATCTTGTAGTCTTGTGCAATGTAACGATGAGTTAGCAACA 399

QY 61 TGCCTTACAAGGAGAGAAAAAGACCGTGCATGCCGATTGGTGAAGTAAAGTGTACGA 120
 DB 400 TGCCTTACAAGGAGAGAAAAAGACCGTGCATGCCGATTGGTGAAGTAAAGTGTACGA 459

QY 121 TCGTGCCTTATTAGGAAGGCAACAGACGGGCTCTGACATGATGATGCAACCACTAAATT 180
 DB 460 TCGTGCCTTATTAGGAAGGCAACAGACGGGCTCTGACATGATGATGCAACCACTAAATT 519

QY 181 CGCATTTGCGAGAGAT-ATTGTATTATTAAGTGCCTGATACATAATAAACGCCATTTCAC 239
 DB 520 CGCATTTGCGAGAGAT-ATTGTATTATTAAGTGCCTGATACATAATAAACGCCATTTCAC 579

QY 240 CATTCAACCACTTGGTGTGCACCTC 264
 DB 580 CATTCAACCACTTGGTGTGCACCTC 604

RESULT 31
 AAQ43814
 ID AAQ43814 standard; DNA; 5750 BP.

XX AC AAQ43814;
 XX DT 25-MAR-2003 (revised)
 XX DT 20-OCT-1993 (first entry)

XX DE pRLD3D4 construct.
 XX KW Epidermal growth factor receptor truncate protein; EGF; binding sites;
 XX KW adsorptive agents; mammalian cell growth abnormality; detection; growth;
 XX KW reproduction; signal transmission; ds.

XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT misc_feature 1077..1079
 XX FT /*tag= a
 XX FT /note= "codon ARA encodes Ile"

XX PN US5218090-A.
 XX PD 08-JUN-1993.
 XX PF 26-OCT-1990; 90US-00604728.
 XX PR 12-JUN-1990; 90US-00536896.
 XX PA (WARN) WARNER LAMBERT CO.
 XX PI Connors RW;
 XX DR WPI; 1993-196297/24.
 XX DR P-ESDB; AAR38211.

XX PT New epidermal growth factor receptor truncate proteins - which bind
 XX PT ligands of EGF receptor without transmitting signal for growth or
 XX PT reproduction.
 XX PS Disclosure; Fig 9; 42pp; English.

QY 61 TGCCTTACAAGGAGAGAAAAAGACCGTGCATGCCGATTGGTGAAGTAAAGTGTACGA 120
 DB 400 TGCCTTACAAGGAGAGAAAAAGACCGTGCATGCCGATTGGTGAAGTAAAGTGTACGA 459

QY 121 TCGTGCCTTATTAGGAAGGCAACAGACGGGCTCTGACATGATGATGCAACCACTAAATT 180
 DB 460 TCGTGCCTTATTAGGAAGGCAACAGACGGGCTCTGACATGATGATGCAACCACTAAATT 519

QY 181 CGCATTTGCGAGAGAT-ATTGTATTATTAAGTGCCTGATACATAATAAACGCCATTTCAC 239
 DB 520 CGCATTTGCGAGAGAT-ATTGTATTATTAAGTGCCTGATACATAATAAACGCCATTTCAC 579

QY 240 CATTCAACCACTTGGTGTGCACCTC 264
 DB 580 CATTCAACCACTTGGTGTGCACCTC 604

RESULT 30
 AAT76802
 ID AAT76802 standard; DNA; 5653 BP.

XX AC AAT76802;
 XX DT 18-NOV-1997 (first entry)

XX DE RSV tar Rev m10 retroviral vector DNA sequence.
 XX KW inhibit; Human Immunodeficiency Virus; HIV; gene expression;
 XX KW transcription activation region; TAR; negative transdominant mutant;
 XX KW Rev M10; mutant; nuclear protein; viral regulatory protein; tat;
 XX KW RSV tar Rev M10 plasmid; Rous sarcoma virus; RSV; ds.

XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT enhancer 37..1129
 XX FT /*tag= b
 XX FT /note= "expression control sequence, contains Rous
 XX FT Sarcoma Virus enhancer and Rev M10 gene"

XX FT CDS 700..1129
 XX FT /*tag= a
 XX FT /note= "Rev M10 gene"

XX PN US5650306-A.
 XX PD 22-JUL-1997.
 XX PF 07-JUN-1993; 93US-00073836.
 XX PR 07-JUN-1993; 93US-00073836.
 XX PA (UNMI) UNIV MICHIGAN.

XX XX Woffendin C, Liu J, Nabel GJ, Yang Z;
 XX WPI; 1997-384672/35.
 XX PT Recombinant nucleic acid for inhibiting HIV gene expression - comprises
 XX PT expression control sequence and transcription activation region linked to
 XX PT rev negative transdominant mutant gene.

XX PS Claim 7; Fig 7; 35pp; English.
 XX CC Recombinant nucleic acid molecules for the improved expression of genes
 XX CC which inhibit Human Immunodeficiency Virus (HIV) gene expression are
 XX CC claimed, which comprise an expression control sequence and a
 XX CC transcription activation region (TAR) sequence, operatively linked to a
 XX CC negative transdominant mutant gene (a protective gene), where the
 XX CC negative transdominant mutant gene is a mutant of rev. Rev is an 18 kDa
 XX CC nuclear viral regulatory protein in HIV gene expression which controls
 XX CC export of viral RNA from the nucleus to the cytoplasm of infected cells.
 XX CC The TAR sequence which is found in the HIV genome controls the regulatory

```

XX CC The sequence is that of the pRLD3D4 construct which encodes the epidermal
CC growth factor (EGF) receptor truncate protein LD3D4 having EGF binding
CC sites. The protein binds ligands of the EGF receptor without transmitting
CC a signal for the growth and reproduction of a cell. It can be used as an
CC adsorptive agent for any moieties that bind the EGF receptor as the
CC portal of entry to a cell. It competes with the EGF receptor present on
CC the cell surface for the binding of ligands and thereby inhibits the
CC action of the ligands or prevents the entry of viruses into cells. It can
CC also be used as for the EGF receptor itself, such as in the detection of
CC abnormalities in mammalian cell growth. It is also useful for prep.
CC novel receptors for efficient detection of ligands and their anti-
CC agonists or agonists. The features table indicate a discrepancy between
CC the LD3D4 protein sequence given in the specification and that which the
CC pRLD3D4 DNA sequence given in the specification would encode. (Updated on
CC 25-MAR-2003 to correct PF field.)
XX SQ Sequence 5750 BP; 1367 A; 1479 C; 1536 G; 1367 T; 0 U; 1 Other;

Query Match          94.0%; Score 248.2; DB 2; Length 5750;
Best Local Similarity 98.5%; Pred. No. 2.1e-76;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGGTAACTAGTGTAGCAACA 60
Db |||||
QY 61 TGCCTTACAGGAGAGAAAAGACACCGTGCATGCGGATTTGTCGAAGTAAAGTGTGTAAGA 120
Db |||||
QY 400 TGCCTTACAGGAGAGAAAAGACACCGTGCATGCGGATTTGTCGAAGTAAAGTGTGTAAGA 459
QY 121 TCGTGCCCTTATTAGGAGGCAACAGACCGGCTCTGACATGGATTCGACATGATTCGACATGATTCGAC 180
Db |||||
QY 460 TCGTGCCCTTATTAGGAGGCAACAGACCGGCTCTGACATGGATTCGACATGATTCGACATGATTCGAC 519
QY 181 CCGCATTGACAGAGAT-ATTGTATTAAAGTGCGCTAGCTCGATACATAAAGCCATTGAC 239
Db |||||
QY 520 CCGCATTGACAGAGATTTATTATTAAAGTGCGCTAGCTCGATACATAAAGCCATTGAC 579
QY 240 CATTCACCACATTTGGTGTGCACCTC 264
Db |||||
QY 580 CATTCACCACATTTGGTGTGCACCTC 604

RESULT 32
AAQ43813
ID AAQ43813 standard; DNA; 6207 BP.
XX AC AAQ43813;
XX DT 25-MAR-2003 (revised)
XX DT 20-OCT-1993 (first entry)
XX DE pRLD2D3D4 construct.
XX KW Epidermal growth factor receptor truncate protein; EGF; binding sites;
XX KW adsorptive agents; mammalian cell growth abnormality; detection; growth;
XX KW reproduction; signal transmission; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX CDS 665..2193
XX FT /*tag= a
XX FT /codon= 707-708 CG encodes Ile
XX FT /note= "encodes LD2D3D4"
XX FT misc_feature 1519..1521
XX FT /*tag= b
XX FT /note= "codon ARA encodes Ile"
XX EN US5218090-A.
XX XX 08-JUN-1993.

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XX PF 26-OCT-1990; 90US-00604728.
XX PR 12-JUN-1990; 90US-00536896.
XX PA (WARN ) WARNER LAMBERT CO.
XX PI Connors RW;
XX DR WPI; 1993-196297/24.
XX DR P-PSDB; AAR38210.
XX PT New epidermal growth factor receptor truncate proteins - which bind
XX PT ligands of EGF receptor without transmitting signal for growth or
XX PT reproduction.
XX FS disclosure; Fig 6; 42pp; English.
XX CC The sequence is that of the pRLD2D3D4 construct which encodes the
XX CC epidermal growth factor (EGF) receptor truncate protein LD2D3D4 having
XX CC EGF binding sites. The protein binds ligands of the EGF receptor without
XX CC transmitting a signal for the growth and reproduction of a cell. It can
XX CC be used as an adsorptive agent for any moieties that bind the EGF
XX CC receptor as the portal of entry to a cell. It competes with the EGF
XX CC receptor present on the cell surface for the binding of ligands and
XX CC thereby inhibits the action of the ligands or prevents the entry of
XX CC viruses into cells. It can also be used as for the EGF receptor itself,
XX CC such as in the detection of abnormalities in mammalian cell growth. It is
XX CC also useful for prep. novel receptors for efficient detection of ligands
XX CC and their anti-agonists or agonists. The features table indicates the
XX CC discrepancies between the LD2D3D4 protein sequence given in the
XX CC specification and that which the pRLD2D3D4 DNA sequence given in the
XX CC specification would encode. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 6207 BP; 1474 A; 1620 C; 1670 G; 1442 T; 0 U; 1 Other;

Query Match          94.0%; Score 248.2; DB 2; Length 6207;
Best Local Similarity 98.5%; Pred. No. 2.2e-76;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGGTAACTAGTGTAGCAACA 60
Db |||||
QY 340 AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGGTAACTAGTGTAGCAACA 399
QY 61 TGCCTTACAGGAGAGAAAAGACACCGTGCATGCGGATTTGTCGAAGTAAAGTGTGTAAGA 120
Db |||||
QY 400 TGCCTTACAGGAGAGAAAAGACACCGTGCATGCGGATTTGTCGAAGTAAAGTGTGTAAGA 459
QY 121 TCGTGCCCTTATTAGGAGGCAACAGACCGGCTCTGACATGGATTCGACATGATTCGACATGATTCGAC 180
Db |||||
QY 460 TCGTGCCCTTATTAGGAGGCAACAGACCGGCTCTGACATGGATTCGACATGATTCGACATGATTCGAC 519
QY 181 CCGCATTGACAGAGAT-ATTGTATTAAAGTGCGCTAGCTCGATACATAAAGCCATTGAC 239
Db |||||
QY 520 CCGCATTGACAGAGATTTATTATTAAAGTGCGCTAGCTCGATACATAAAGCCATTGAC 579
QY 240 CATTCACCACATTTGGTGTGCACCTC 264
Db |||||
QY 580 CATTCACCACATTTGGTGTGCACCTC 604

RESULT 33
AAQ43812
ID AAQ43812 standard; DNA; 6274 BP.
XX AC AAQ43812;
XX DT 25-MAR-2003 (revised)
XX DT 20-OCT-1993 (first entry)
XX DE pRLD1D2D3 .Apal construct.
XX KW Epidermal growth factor receptor truncate protein; EGF; growth;

```

KW binding sites; adsorptive agents; mammalian cell growth abnormality;
 KW detection; reproduction; signal transmission; pRLD1D2D3Apal; ds.
 XX Synthetic.

XX Key Location/Qualifiers
 PH 665..2253
 FT CDS
 FT /tag= a
 FT /codon= 707-708 CG encodes Ile
 FT /note= "encodes LpD1D2D3Apal"
 FT 1939..1941
 FT /tag= b
 FT /note= "codon ARA encodes Ile"

XX US5218090-A.
 XX 08-JUN-1993.
 XX 26-OCT-1990; 90US-00604728.
 XX 12-JUN-1990; 90US-00536896.
 XX (WARN) WARNER LAMBERT CO.
 XX Connors RW;
 XX WPI; 1993-196297/24.
 DR F-PSDB; AAR38209.

XX New epidermal growth factor receptor truncate proteins - which bind
 PT ligands of EGF receptor without transmitting signal for growth or
 PT reproduction..

XX Disclosure; Fig 3; 42pp; English.

XX The sequence is that of the pRLD1D2D3 construct which encodes the
 CC epidermal growth factor (EGF) receptor truncate protein LpD1D2D3Apal.
 CC having EGF binding sites. The protein binds ligands of the EGF receptor
 CC without transmitting a signal for the growth and reproduction of a cell.
 CC It can be used as an adsorptive agent for any moieties that bind the EGF
 CC receptor as the portal of entry to a cell. It competes with the EGF
 CC thereby inhibits the action of the ligands or prevents the entry of
 CC viruses into cells. It can also be used as for the EGF receptor itself,
 CC such as in the detection of abnormalities in mammalian cell growth. It is
 CC also useful for preps. novel receptors for efficient detection of ligands
 CC and their anti-agonists or agonists. The features table indicates the
 CC discrepancies between the LpD1D2D3 protein sequence given in the
 CC specification and that which the pRLD1D2D3 DNA sequence given in the
 CC specification would encode. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 6274 BP; 1506 A; 1610 C; 1664 G; 1493 T; 0 U; 1 Other;
 Query Match 94.0%; Score 248.2; DB 2; Length 6274;
 Best Local Similarity 98.5%; Pred. No. 2.2e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATCTAGCTTTATGCAATACACTTTGTTAGTCTTGTGCAATGTTAAGTGGTACCA 60
 DB 340 AATGAGCTTTATGCAATACACTTTGTTAGTCTTGTGCAATGTTAAGTGGTACCA 399
 QY 61 TGCCTTACAGGAGAGAAAAGACCGGTGTCATGCGATTGGTGGAGTAAAGTGGTACCA 120
 DB 400 TGCCTTACAGGAGAGAAAAGACCGGTGTCATGCGATTGGTGGAGTAAAGTGGTACCA 459
 QY 121 TCGTGCCTTTATGAGAGGAAAAGACCGGTGTCATGCGATTGGTGGAGTAAAGTGGTACCA 180
 DB 460 TCGTGCCTTTATGAGAGGAAAAGACCGGTGTCATGCGATTGGTGGAGTAAAGTGGTACCA 519
 QY 181 CGCATTGCGAGAGAT-ATTGATTATTAGTGCCTTACCTGATGATACATTAACGCCATTGAC 239
 DB 520 CGCATTGCGAGAGATATTGATTATTAGTGCCTTACCTGATGATACATTAACGCCATTGAC 579

QY 240 CATTACACACATTGTTGTGCACCTC 264
 DB 580 CATTACACACATTGTTGTGCACCTC 604

RESULT 34
 AAA53869
 ID AAA53869 standard; DNA; 6838 BP.
 XX
 AC AAA53869;
 XX
 DT 03-JAN-2001 (first entry)
 XX
 DE Expression vector pRIG-1.

XX Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 XX Synthetic.

XX WO2000049162-A2.
 XX 24-AUG-2000.
 XX 22-FEB-2000; 2000WC-US004429.
 XX 19-FEB-1999; 99US-00253022.
 PR 08-MAR-1999; 99US-00263814.
 PR 26-MAR-1999; 99US-00276820.
 XX
 PA (ATHE-) ATHERSYS INC.

XX Harrington JJ, Sherf B, Rundlett S;
 XX WPI; 2000-549276/50.

XX Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.

XX Example 1; Fig 14; 240pp; English.

XX New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known

XX Sequence 6838 BP; 1679 A; 1669 C; 1709 G; 1781 T; 0 U; 0 Other;
 Query Match 94.0%; Score 248.2; DB 3; Length 6838;
 Best Local Similarity 98.5%; Pred. No. 2.3e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGAGCTTTATGCAATACACTTTGTTAGTCTTGTGCAATGTTAAGTGGTACCA 60
 DB 1559 AATGAGCTTTATGCAATACACTTTGTTAGTCTTGTGCAATGTTAAGTGGTACCA 1618
 QY 61 TGCCTTACAGGAGAGAAAAGACCGGTGTCATGCGATTGGTGGAGTAAAGTGGTACCA 120
 DB 1619 TGCCTTACAGGAGAGAAAAGACCGGTGTCATGCGATTGGTGGAGTAAAGTGGTACCA 1678
 QY 121 TCGTGCCTTTATGAGAGGAAAAGACCGGTGTCATGCGATTGGTGGAGTAAAGTGGTACCA 190

Db 1679 TCGTGCCCTTATTAGGAAGGCAACAGACAGGCTCTGACATGGATTGCGACGAACCACTGAATT 1738
 QY 181 CGCATTCGACAGAT-ATTGTATTATTAGTCCCTAGCTGATACATATAAAGCCATTGAC 239
 Db 1739 CGCATTCGACAGATATTGTATTAAAGTCCCTAGCTGATACATATAAAGCCATTGAC 1798
 QY 240 CATTCCACACATTGGTGTGCACCTC 264
 Db 1799 CATTCCACACATTGGTGTGCACCTC 1823
 RESULT 35
 AAT84562
 ID AAT84562 standard; cDNA; 8591 BP.
 AC AAT84562;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-DEC-1997 (first entry)
 XX
 DE Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;
 KW cyclic.
 OS Homo; sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 2393..3856
 FT /*tag= a
 XX
 XX US5652092-A.
 XX 29-JUL-1997.
 XX
 XX 05-JUN-1995; 95US-00462859.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobson JS, Vitek MP;
 XX
 DR WPI; 1997-392937/36.
 DR P-PSDB; AAW26394.
 XX
 XX Screening for compounds which reduce beta-amyloid protein formation -
 PT using cells which express a construct encoding a marker and an amyloid
 PT precursor muten derived from APP isoforms.
 XX
 PS Disclosure; Fig 8; 84pp; English.
 XX
 XX Plasmid pCLL621 (AAT84562), deposited in E. coli as ATCC 69406, codes
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26394), that has a 276-amino acid deletion of the native APP and
 CC carries a substance P epitope marker on the N-terminal side of the beta-
 CC amyloid protein (BAP) domain. APP-REP 751 can be used in a claimed method
 CC for screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
 Query Match 94.08; Score 248.2; DB 2; Length 8591;
 Best Local Similarity 98.58; Pred. No. 2.5e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTCAACATGCTTAACGATGAGTTAGCAACA 60
 Db 4975 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTCAACATGCTTAACGATGAGTTAGCAACA 5034
 QY 61 TGCCTTACAGGAGAGAAAAGACACCGTGCATGCCATTCGTCGAGTGGAGTGGTACGA 120
 Db 5035 TGCCTTACAGGAGAGAAAAGACACCGTGCATGCCATTCGTCGAGTGGAGTGGTACGA 5094
 QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACAGGCTCTGACATGGATTGCGACGAACCACTGAATT 180
 Db 5095 TCGTGCCCTTATTAGGAAGGCAACAGACAGGCTCTGACATGGATTGCGACGAACCACTGAATT 5154
 QY 181 CGCATTCGACAGAT-ATTGTATTATTAGTCCCTAGCTGATACATATAAAGCCATTGAC 239
 Db 5155 CGCATTCGACAGATATTGTATTAAAGTCCCTAGCTGATACATATAAAGCCATTGAC 5214
 QY 240 CATTCCACACATTGGTGTGCACCTC 264
 Db 5215 CATTCCACACATTGGTGTGCACCTC 5239
 RESULT 36
 AAT84561
 ID AAT84561 standard; cDNA; 8591 BP.
 XX
 AC AAT84561;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-DEC-1997 (first entry)
 XX
 DE Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;
 KW cyclic.
 OS Homo; sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 2393..3871
 FT /*tag= a
 XX
 XX US5652092-A.
 XX 29-JUL-1997.
 XX
 XX 05-JUN-1995; 95US-00462859.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobson JS, Vitek MP;
 XX
 DR WPI; 1997-392937/36.
 DR P-PSDB; AAW26393.
 XX
 XX Screening for compounds which reduce beta-amyloid protein formation -
 PT using cells which express a construct encoding a marker and an amyloid
 PT precursor muten derived from APP isoforms.
 XX
 PS Disclosure; Fig 7; 84pp; English.
 XX
 XX Plasmid pCLL602 (AAT84561), deposited in E. coli as ATCC 69405, codes

CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26393), that has a 276-amino acid deletion of the native APP and
 CC carries Substance P and Met-enkephalin epitope markers placed,
 CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid
 CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for
 CC screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 2; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 2.5e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 5034
 QY 61 TGCCTTACAGGAGAGAAAAGAACCCGTCGATGCGGATTTGGTGAAGTAAAGTGTGACGA 120
 DB 5035 TGCCTTACAGGAGAGAAAAGAACCCGTCGATGCGGATTTGGTGAAGTAAAGTGTGACGA 5094
 QY 121 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGATTTGACAGACCACTAAATT 180
 DB 5095 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGATTTGACAGACCACTAAATT 5154
 QY 181 CCGCATTCGACAGAT-ATTGTATTTAAGTCTAGCTCGATACATATACGCAATTTGAC 239
 DB 5155 CCGCATTCGACAGATTAATTGTATTAAAGTGCCTAGCTCGATACATATACGCAATTTGAC 5214
 QY 240 CATTCACCACTTGTGTGCACCTC 264
 DB 5215 CATTCACCACTTGTGTGCACCTC 5239

RESULT 37
 AAT87083
 ID AAT87083 standard; cDNA; 8591 BP.
 XX
 AC AAT87083;
 XX
 DT 25-MAR-2003 (revised)
 DT 06-JAN-1998 (first entry)
 XX
 DE Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;
 KW cyclic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FE Key Location/Qualifiers
 FT CDS 2393..3871
 FT /*tag= a
 XX
 XX US5656477-A.
 XX
 PD 12-AUG-1997.
 XX
 XX 20-SEP-1993; 93US-00123659.
 XX
 XX 01-MAY-1992; 92US-00877675.

XX (AMCY) AMERICAN CYANAMID CO.
 PA Jacobeen JS, Vitek MP;
 XX
 DR WPI; 1997-414594/38.
 DR P-PSDB; AAW26509.
 XX
 PT Nucleic acid encoding amyloid precursor muten(s) - comprising reporter
 PT gene and coding sequence, for identifying compounds which modify the
 PT activity of proteolytic enzymes which cleave APP.
 XX
 DT Disclosure; Fig 7; 84pp; English.

CC Plasmid pCLL602 (AAW87083), deposited in E. coli as ATCC 69405, codes
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26509), that has a 276-amino acid deletion of the native APP and
 CC carries Substance P and Met-enkephalin epitope markers placed,
 CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid
 CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for
 CC screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
 Query Match 94.0%; Score 248.2; DB 2; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 2.5e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 60
 DB 4975 AATGTAGTCTTATGCAATACACTTGTAGTCTTGTGCAATGCTTAACGATGAGTTAGCAACA 5034
 QY 61 TGCCTTACAGGAGAGAAAAGAACCCGTCGATGCGGATTTGGTGAAGTAAAGTGTGACGA 120
 DB 5035 TGCCTTACAGGAGAGAAAAGAACCCGTCGATGCGGATTTGGTGAAGTAAAGTGTGACGA 5094
 QY 121 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGATTTGACAGACCACTAAATT 180
 DB 5095 TCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGATTTGACAGACCACTAAATT 5154
 QY 181 CCGCATTCGACAGAT-ATTGTATTTAAGTCTAGCTCGATACATATACGCAATTTGAC 239
 DB 5155 CCGCATTCGACAGATTAATTGTATTAAAGTGCCTAGCTCGATACATATACGCAATTTGAC 5214
 QY 240 CATTCACCACTTGTGTGCACCTC 264
 DB 5215 CATTCACCACTTGTGTGCACCTC 5239

RESULT 38
 AAT87084
 ID AAT87084 standard; cDNA; 8591 BP.
 XX
 AC AAT87084;
 XX
 DT 25-MAR-2003 (revised)
 DT 06-JAN-1998 (first entry)
 XX
 DE Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;
 KW cyclic.
 XX

QY	121	TGTTGCTTTATTAGGAAGCAACAGACGGGTCTGACATGATTTGGACCAACCACTAAATT	180
Db	5095	TGTTGCTTTATTAGGAAGCAACAGACGGGTCTGACATGATTTGGACCAACCACTGAATT	5154
QY	181	CGCATTCGACAGAT-ATTGTATTATTAAAGTGGCTAGCTCGATACAAATAAAGGCCATTTCAC	239
Db	5155	CGCATTCGACAGATATTGTATTATTAAAGTGGCTAGCTCGATACAAATAAAGGCCATTTCAC	5214
QY	240	CATTCAACACATTGGTGTGCACCTC	264
Db	5215	CATTCAACACATTGGTGTGCACCTC	5239
RESULT 40			
AAV04865	ID	AAV04865 standard; DNA; 8591 BP.	
XX	AC	AAV04865;	
DT	01-MAY-1998	(first entry)	
DE	cDNA encoding amyloid precursor protein mutant APP-APP 75i.		
XX	Beta-amyloid peptide; BAP; extracellular BAP plaque;		
KW	cerebrovascular deposit; Alzheimers disease; Downs syndrome;		
KW	amyloid precursor protein; APP; secretase; BAP aggregation;		
KW	abnormal proteolytic cleavage; ds.		
XX			
OS	Homo sapiens.		
XX			
FF	Key	Location/Qualifiers	
FT	CDS	2393..3871	
FT		/*tag= a	
XX			
PN	US5703209-A.		
XX			
PD	30-DEC-1997.		
XX			
PF	05-JUN-1995;	95US-00464248.	
XX			
PR	01-MAY-1992;	92US-00877675.	
PR	20-SEP-1993;	93US-00123659.	
XX	(AMCY) AMERICAN CYANAMID CO.		
PA			
XX			
PI	Jacobseen JS, Vitek MP;		
XX			
DR	WPI; 1998-076482/07.		
DR	P-PSDB; AAW42978.		
XX			
PT	Amyloid precursor protein fusion polypeptides - comprising APP fragment		
PT	and marker, useful for research and drug screening.		
XX			
PS	Disclosure; Fig 7A-Q; 84pp; English.		
XX			
CC	The present sequence encodes an amyloid precursor protein (APP), which		
CC	has a deletion of 276 amino acids to within 15 amino acids of the beta-		
CC	amyloid peptide (BAP) domain. The protein also contains the Met-		
CC	enkephalin reporter epitope at the carboxy terminus. Abnormal		
CC	accumulation of extracellular BAP in plaques and cerebrovascular deposits		
CC	is characteristic in brains of individuals suffering from Alzheimers		
CC	disease and Downs syndrome. BAP is a poorly soluble, self-aggregating		
CC	protein which is derived from a larger amyloid precursor protein (APP).		
CC	APP is expressed as an integral membrane protein, and is cleaved by		
CC	secretase, between BAP 161ys and 171Leu. Cleavage at this site precludes		
CC	amyloidogenesis and results in the release of the amino-terminal APP		
CC	fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-		
CC	770. These isoforms are derived by alternative splicing. APP-RP 751 is		
CC	constructed by ligating restriction fragments representing N- and C-		
CC	terminal APP-751 cDNA and substrate P reporter epitope sequences. APP		
CC	can be used as a substrate for studying abnormal proteolytic cleavage		
CC	which results in the release of BAP, and also to screen for drugs that		

CC	will inhibit such cleavage
XX	
XX	sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
QQ	
Query Match	94.0%; Score 248.2; DB 2; Length 8591;
Best Local Similarity	98.5%; Pred. No. 2.5e-76;
Matches 261; Conservative	0; Mismatches 3; Indels 1; Gaps 1;
QY	1 AATGTAAGTCTTAATGCAATACACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAACA 60
DB	4975 AATGTAAGTCTTAATGCAATACACTCTTGTAGTCTTGCAACATGGTAACGATGAGTTAGCAACA 5034
QY	61 TGCCTTACAAGGAGAGAAAGACACCGTGCATGCCGATTGTTGGAAAGTAAAGTGGTACGA 120
DB	5035 TGCCTTACAAGGAGAGAAAGACACCGTGCATGCCGATTGTTGGAAAGTAAAGTGGTACGA 5094
QY	121 TCGTGCCCTTATTTAGGAAGGCAAGACAGCGGCTCTGACATGGATTGGACGACACTAAATT 180
DB	5095 TCGTGCCCTTATTTAGGAAGGCAAGACAGCGGCTCTGACATGGATTGGACGAAACCACTGAATT 5154
QY	181 CGGCATTGCAGAGAT-ATTGTAATTTAAGTGCTAGCTGCATACATAAAGCCATTTCAC 2339
DB	5155 CGGCATTGCAGAGATATTGTAATTTAAGTGCTAGCTGCATACATAAAGCCATTTCAC 5214
QY	240 CATTCACCACATTGGTGTGCACCTC 264
DB	5215 CATTCACCACATTGGTGTGCACCTC 5239
RESULT 41	
AAV05850	
ID	AAV05850 standard; cDNA; 8591 BP.
AC	AAV05850;
AD	
DT	01-JUN-1998 (first entry)
DE	APP-REP 751 gene from pCLL621.
KW	Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
KW	epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
KW	Alzheimer's disease; cleavage; cyclic; circular; ds.
OS	Homo sapiens.
OS	Synthetic.
FX	
FX	Key Location/Qualifiers
FT	2393..3856
FT	/*tag= a
FT	/product= "APP-REP_751"
XX	
PN	US5693478-A.
PD	
PD	02-DEC-1997.
XX	
XX	05-JUN-1995; 95US-00464247.
XX	
PR	01-MAY-1992; 92US-00877675.
PR	20-SEP-1993; 93US-00123659.
XX	
PA	(AMCY) AMERICAN CYANAMID CO.
PI	
PI	Jacobsen JS, Vitek MP;
DR	WPI; 1998-031744/03.
DR	P-PSDB; AAM44745.
XX	
PT	Amyloid precursor mutin reporter molecule assay containing antibody
PT	recognised marker - used to study pathways associated with Alzheimer's
PT	disease.
XX	
PS	Disclosure; Fig 8; 84pp; English.
XX	

CC This is the nucleotide sequence encoding a novel amyloid precursor
 CC protein (APP) designated APP-REP 751, contained in construct pC1621. The
 CC sequence encodes a mutant version of the APP 751 isoform of human APP
 CC which contains a deletion of 276 amino acids from the central region. The
 CC deleted region is replaced by a substrate P reporter epitope sequence
 CC (RPPQDFGLM). In contrast to the APP-REP 751 encoded by the construct
 CC pC1621 (AAV05849), this sequence does not contain a Met-enkephalin
 CC reporter epitope (YGGFM) fused at the C-terminus of the coding sequence.
 CC The shorter protein is generated for ease of detection based on size
 CC difference with the wild type APP protein and also by detection of the
 CC reporter epitopes. The mutant protein can be used in a method to study
 CC secretase and beta-amyloid protein (BAP)-generating pathways associated
 CC with Alzheimer's disease by studying proteolytic cleavage of the reporter
 CC polypeptides
 XX
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2248 G; 2080 T; 0 U; 0 Other;

Query Match 94.0%; Score 248.2; DB 2; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 2.5e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCATGTTGGAAGTGAAGTGGTACGA 60
 DB 4975 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCATGTTGGAAGTGAAGTGGTACGA 5034
 QY 61 TGCCTTACAGGAGAGAAAAAGCACCCTGTCATGCGGATTTGGTGAAGTGAAGTGGTACGA 120
 DB 5035 TGCCTTACAGGAGAGAAAAAGCACCCTGTCATGCGGATTTGGTGAAGTGAAGTGGTACGA 5094
 QY 121 TCGTGCCTTATAGGAGGCAACAGACGGGTCTGCATGATGGAAGTGAAGTGGTACGA 180
 DB 5095 TCGTGCCTTATAGGAGGCAACAGACGGGTCTGCATGATGGAAGTGAAGTGGTACGA 5154
 QY 181 CCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGAC 239
 DB 5155 CCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGAC 5214
 QY 240 CATTACACCATTTGGTGGCACCTC 264
 DB 5215 CATTACACCATTTGGTGGCACCTC 5239

RESULT 42
 AAV05849
 ID AAV05849 standard; cDNA; 8591 BP.
 XX
 AC AAV05849;
 XX
 DT 01-JUN-1998 (first entry)
 XX
 DE APP-REP 751 gene from pC1621.
 XX
 KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
 KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
 KW Alzheimer's disease; cleavage; cyclic; circular; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 EH Key Location/Qualifiers
 FT CDS 2393..3871
 FT /*tag= a
 FT /*product= "APP_REP_751"
 XX
 PN US5693478-A.
 PD 02-DEC-1997.
 XX
 PF 05-JUN-1995; 95US-00464247.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX

PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR MPI; 1998-031744/03.
 DR P-PSDB; AAM44744.
 XX
 PT Amyloid precursor mutin reporter molecule assay containing antibody
 PT recognised marker - used to study pathways associated with Alzheimer's
 PT disease.
 XX
 PS Disclosure; Fig 7; 84pp; English.
 XX
 CC This is the nucleotide sequence encoding a novel amyloid precursor
 CC protein (APP) designated APP-REP 751, contained in construct pC1621. The
 CC sequence encodes a mutant version of the APP 751 isoform of human APP
 CC which contains a deletion of 276 amino acids from the central region. The
 CC deleted region is replaced by a substrate P reporter epitope sequence
 CC (RPPQDFGLM) and a Met-enkephalin reporter epitope (YGGFM) is fused at
 CC the C-terminus. The shorter protein is generated for ease of detection
 CC based on size difference with the wild type APP protein and also by
 CC detection of the reporter epitopes. The mutant protein can be used in a
 CC method to study secretase and beta-amyloid protein (BAP)-generating
 CC pathways associated with Alzheimer's disease by studying proteolytic
 CC cleavage of the reporter polypeptides
 XX
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
 Query Match 94.0%; Score 248.2; DB 2; Length 8591;
 Best Local Similarity 98.5%; Pred. No. 2.5e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCATGTTGGAAGTGAAGTGGTACGA 60
 DB 4975 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCATGTTGGAAGTGAAGTGGTACGA 5034
 QY 61 TGCCTTACAGGAGAGAAAAAGCACCCTGTCATGCGGATTTGGTGAAGTGAAGTGGTACGA 120
 DB 5035 TGCCTTACAGGAGAGAAAAAGCACCCTGTCATGCGGATTTGGTGAAGTGAAGTGGTACGA 5094
 QY 121 TCGTGCCTTATAGGAGGCAACAGACGGGTCTGCATGATGGAAGTGAAGTGGTACGA 180
 DB 5095 TCGTGCCTTATAGGAGGCAACAGACGGGTCTGCATGATGGAAGTGAAGTGGTACGA 5154
 QY 181 CCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGAC 239
 DB 5155 CCGCATTCGACAGAT-ATTGTATTTAAGTGCCTAGCTCGATACATAAAGCCATTGAC 5214
 QY 240 CATTACACCATTTGGTGGCACCTC 264
 DB 5215 CATTACACCATTTGGTGGCACCTC 5239

RESULT 43
 ABL57333
 ID ABL57333 standard; DNA; 8902 BP.
 XX
 AC ABL57333;
 XX
 DT 29-AUG-2003 (revised)
 DT 09-AUG-2002 (first entry)
 XX
 DE Vector plasmid pRIG-MP1.
 XX
 KW Vector; pRIG-MP1; promoter; ds.
 XX
 OS Cytomegalovirus.
 OS Escherichia coli.
 OS Rhesus macaque polyoma virus.
 OS Rous sarcoma virus.
 OS Chimeric.
 XX
 PN US2002055172-A1.

Db 1648 CATTACACACATTGGTGTGCACCTC 1672

RESULT 45
 AAA53879
 ID AAA53879 standard; DNA; 9732 BP.
 XX
 AC AAA53879;
 XX
 DT 03-JAN-2001 (first entry)
 XX
 DE Expression vector pRIG-TP.
 XX
 KW Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 XX
 OS Synthetic.
 XX
 FN WO200049162-A2.
 XX
 PD 24-AUG-2000.
 XX
 PF 22-FEB-2000; 2000WO-US004429.
 XX
 PR 19-FEB-1999; 99US-00253022.
 PR 08-MAR-1999; 99US-00263814.
 PR 26-MAR-1999; 99US-00276820.
 XX
 PA (ATHE-) ATHERSYS INC.
 XX
 PI Harrington JJ, Sherf B, Rundlett S;
 XX
 DR WPI; 2000-549276/50.
 XX
 PT Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.
 XX
 PS Example 15; Fig 37; 240pp; English.
 XX
 CC New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known
 XX
 SQ Sequence 9732 BP; 2427 A; 2512 C; 2443 G; 2348 T; 0 U; 2 Other;
 Query Match 94.0%; Score 248.2; DB 3; Length 9732;
 Best Local Similarity 98.5%; Pred. No. 2.7e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGGTAAAGTAGTAGCAACA 60
 Db 1411 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGGTAAAGTAGTAGCAACA 1470
 QY 61 TGCCTTACAGGAGAGAAAAGACCCGTCATCCGATGGTGAAGTAGGTAGCA 120
 Db 1471 TGCCTTACAGGAGAGAAAAGACCCGTCATCCGATGGTGAAGTAGGTAGCA 1530
 QY 121 TGTGCTCCCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGCGAACCACTAAATT 180
 Db 1531 TGTGCTCCCTTATTAGGAGGCAACAGACAGGTCTGACATGGATTGCGAACCACTGAATT 1590

QY 181 CCGCATTCGAGAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATTAACCGCATTTGAC 239
 Db 1591 CCGCATTCGAGAGATAATGTATTTAAGTGGCTAGCTCGATACATTAACCGCATTTGAC 1650

QY 240 CATTACACACATTGGTGTGCACCTC 264
 Db 1651 CATTACACACATTGGTGTGCACCTC 1675

RESULT 46
 AAA53874
 ID AAA53874 standard; DNA; 9738 BP.
 XX
 AC AAA53874;
 XX
 DT 03-JAN-2001 (first entry)
 XX
 DE Expression vector pRIG20.
 XX
 KW Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 XX
 OS Synthetic.
 XX
 FN WO200049162-A2.
 XX
 PD 24-AUG-2000.
 XX
 PF 22-FEB-2000; 2000WO-US004429.
 XX
 PR 19-FEB-1999; 99US-00253022.
 PR 08-MAR-1999; 99US-00263814.
 PR 26-MAR-1999; 99US-00276820.
 XX
 PA (ATHE-) ATHERSYS INC.
 XX
 PI Harrington JJ, Sherf B, Rundlett S;
 XX
 DR WPI; 2000-549276/50.
 XX
 PT Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.
 XX
 PS Disclosure; Fig 31; 240pp; English.
 XX
 CC New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known
 XX
 SQ Sequence 9738 BP; 2428 A; 2514 C; 2447 G; 2347 T; 0 U; 2 Other;
 Query Match 94.0%; Score 248.2; DB 3; Length 9738;
 Best Local Similarity 98.5%; Pred. No. 2.7e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGGTAAAGTAGTAGCAACA 60
 Db 1411 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGGTAAAGTAGTAGCAACA 1470

QY 61 TGCCTTACAGGAGAGAAAGCAACCGTCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 120
 DB 1471 TGCCTTACAGGAGAGAAAGCAACCGTCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 1530
 QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGCTCTGCATGGAATTTGGAGCAACCACTAAATT 180
 DB 1531 TCGTGCCCTTATTAGGAGGCAACAGACGGCTCTGCATGGAATTTGGAGCAACCACTAAATT 1590
 QY 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAAAGCGCAATTGAC 239
 DB 1591 CGCATTGCGAGAGATTAATTGATTAAAGTGCCTAGCTCGATACATAATAAAGCGCAATTGAC 1650
 QY 240 CATTACACCAATTGGTGTGCACCTC 264
 DB 1651 CATTACACCAATTGGTGTGCACCTC 1675

RESULT 47

AAA53875
 ID AAA53875 standard; DNA; 9873 BP.
 AC AAA53875;
 XX

DT 03-JAN-2001 (first entry)
 DE Expression vector pRIGadi.

XX Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 XX Synthetic.
 XX

PN WC200049162-A2.
 XX

PD 24-AUG-2000.
 XX

PF 22-FEB-2000; 2000WC-US004429.
 XX

PR 19-FEB-1999; 99US-00253022.
 PR

PR 08-MAR-1999; 99US-00263814.
 PR

PR 26-MAR-1999; 99US-00276820.
 XX

XX (ATHE-) ATHERSYS INC.
 PA

XX Harrington JJ, Sherf B, Rundlett S;
 FI

XX WPI; 2000-549276/50.
 XX

XX Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.

XX Disclosure; Fig 32; 240pp; English.
 PS

XX New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known
 XX

SQ Sequence 9873 BP; 2450 A; 2557 C; 2501 G; 2363 T; 0 U; 2 Other;

Query Match

94.0%; Score 248.2; DB 3; Length 9873;

Best Local Similarity 98.5%; Pred. No. 2.7e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTGTAACGATGAGTTAGCAACA 60

DB 1550 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTGTAACGATGAGTTAGCAACA 1609

QY 61 TGCCTTACAGGAGAGAAAGCAACCGTCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 120

DB 1610 TGCCTTACAGGAGAGAAAGCAACCGTCATGCCGATTTGGTGGAAAGTAAGTGGTACGA 1669

QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGCTCTGCATGGAATTTGGAGCAACCACTAAATT 180

DB 1670 TCGTGCCCTTATTAGGAGGCAACAGACGGCTCTGCATGGAATTTGGAGCAACCACTAAATT 1729

QY 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAATAAAGCGCAATTGAC 239

DB 1730 CGCATTGCGAGAGATTAATTGATTAAAGTGCCTAGCTCGATACATAATAAAGCGCAATTGAC 1789

QY 240 CATTACACCAATTGGTGTGCACCTC 264

DB 1790 CATTACACCAATTGGTGTGCACCTC 1814

RESULT 48

AAA53876

ID AAA53876 standard; DNA; 10054 BP.

AC AAA53876;
 XX

DT 03-JAN-2001 (first entry)
 DE Expression vector pRIGadi.

XX Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 XX Synthetic.
 XX

PN WC2000049162-A2.
 XX

PD 24-AUG-2000.
 XX

PF 22-FEB-2000; 2000WC-US004429.
 XX

PR 19-FEB-1999; 99US-00253022.
 PR

PR 08-MAR-1999; 99US-00263814.
 PR

PR 26-MAR-1999; 99US-00276820.
 XX

XX (ATHE-) ATHERSYS INC.
 PA

XX Harrington JJ, Sherf B, Rundlett S;
 FI

XX WPI; 2000-549276/50.
 XX

XX Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.
 XX Disclosure; Fig 33; 240pp; English.

XX New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous

CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known
 XX
 SQ Sequence 10054 BP; 2548 A; 2562 C; 2515 G; 2427 T; 0 U; 2 Other;
 Query Match 94.0%; Score 248.2; DB 3; Length 10054;
 Best Local Similarity 98.5%; Pred. No. 2.7e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAGTGTAGTGTAGCAACA 60
 DB 1733 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAGTGTAGTGTAGCAACA 1792
 QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATGTTGCGAAGTGTAGTGTAGCAACA 120
 DB 1793 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATGTTGCGAAGTGTAGTGTAGCAACA 1852
 QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGCGGTCTGCATGCGATTGGACGACCACTAAATT 180
 DB 1853 TCGTGCCCTTATTAGGAAGGCAACAGACAGGTCTGCATGCGATTGGACGACCACTAAATT 1912
 QY 181 CCGCATTGCGAGAGAT-ATTGTATTTAAGTGTGCTAGTGTGCAATTAACGCCATTGTGAC 239
 DB 1913 CCGCATTGCGAGAGAT-ATTGTATTTAAGTGTGCTAGTGTGCAATTAACGCCATTGTGAC 1972
 QY 240 CATTCCACCATTTGGTGTGCACCTC 264
 DB 1973 CATTCCACCATTTGGTGTGCACCTC 1997
 RESULT 49
 AAV59501
 ID AAV59501 standard; DNA; 11265 BP.
 XX
 AC AAV59501;
 XX
 DT 17-OCT-2003 (revised)
 DT 02-FEB-1999 (first entry)
 XX
 DE Plasmid pREP7::CTLA4-hIg.
 XX
 KW pREP7::CTLA4-hIg; plasmid; CTLA4; immunoglobulin; vaccine;
 KW DNA immunisation; human; mouse; ds; circular; cyclic.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 PN W09844129-A1.
 XX
 PD 06-OCT-1998.
 XX
 PF 26-MAR-1998; 98WO-AU000208.
 XX
 PR 27-MAR-1997; 97AU-00005891.
 PR 13-FEB-1998; 98AU-00001830.
 XX
 PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UYWE) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (CSLC-) CSL LTD.
 XX
 PI Boyle JS, Brady JL, Lew AM;
 XX
 DR WPI; 1998-557122/47.
 XX
 PT DNA molecule for raising an immune response to antigen - comprises
 PT sequence encoding dimerisation or multimerisation polypeptide.
 XX
 PS Disclosure; Page 32-37; 64pp; English.
 XX

CC This is the DNA sequence of expression plasmid pREP7::CTLA4-hIg that
 CC encodes a secreted form of the Fc fragment of human IgG1 fused to murine
 CC CTLA4. The invention provides a new DNA molecule for use in raising an
 CC immune response to an antigen. The DNA molecule comprises: (i) a first
 CC sequence encoding a targeting molecule (e.g. CTLA4, which acts as a
 CC targeting molecule to antigen-presenting cells expressing B-7); (ii) a
 CC second sequence encoding the antigen or its epitope, and (iii) optionally
 CC a third sequence encoding a polypeptide (e.g. an immunoglobulin) which
 CC promotes dimerisation or multimerisation of the product encoded by the
 CC DNA molecule. Also claimed are a polypeptide encoded by the DNA molecule,
 CC and a vector including the DNA molecule. The inventors have shown that
 CC fusion proteins consisting of antigen and cell surface receptor ligands
 CC can deliver antigen to sites of immune induction which enhance the immune
 CC response and possibly the efficacy of genetic vaccines. The DNA molecule
 CC can be used in a claimed method for deviating an immune response to an
 CC antigen in an individual. (Updated on 17-OCT-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 11265 BP; 2717 A; 2979 C; 3002 G; 2567 T; 0 U; 0 Other;
 Query Match 94.0%; Score 248.2; DB 2; Length 11265;
 Best Local Similarity 98.5%; Pred. No. 2.9e-76;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAGTGTAGTGTAGCAACA 60
 DB 369 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGTTAGTGTAGTGTAGCAACA 428
 QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATGTTGCGAAGTGTAGTGTAGCAACA 120
 DB 429 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATGTTGCGAAGTGTAGTGTAGCAACA 488
 QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGCGGTCTGCATGCGATTGGACGACCACTAAATT 180
 DB 489 TCGTGCCCTTATTAGGAAGGCAACAGACAGGTCTGCATGCGATTGGACGACCACTAAATT 548
 QY 181 CCGCATTGCGAGAGAT-ATTGTATTTAAGTGTGCTAGTGTGCAATTAACGCCATTGTGAC 239
 DB 549 CCGCATTGCGAGAGAT-ATTGTATTTAAGTGTGCTAGTGTGCAATTAACGCCATTGTGAC 608
 QY 240 CATTCCACCATTTGGTGTGCACCTC 264
 DB 609 CATTCCACCATTTGGTGTGCACCTC 633
 RESULT 50
 AAL55269
 ID AAL55269 standard; DNA; 16958 BP.
 XX
 AC AAL55269;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE DNA of expression vector RC77, SEQ ID No 3.
 XX
 KW Vector; excisable; site-specific recombinase; enzyme; exogenous;
 KW signalling molecule; transcription factor; cell metabolism;
 KW differentiation state; kinase; phosphatase; ds.
 XX
 OS Unidentified.
 XX
 PN W02003002735-A2.
 XX
 PD 09-JAN-2003.
 XX
 PF 28-JUN-2002; 2002WO-CA000997.
 XX
 PR 28-JUN-2001; 2001US-0301149P.
 XX
 PA (PHEN-) PHENOGENE THERAPEUTICS INC.
 XX
 PI Lanctot C, Gingras R, Gaumond M;
 XX

PN US5589392-A.
 XX 31-DEC-1996.
 XX 29-NOV-1993; 93US-00158718.
 XX 14-JAN-1991; 91US-00640983.
 XX (STRA-) STRATAGENE.
 XX Short JM;
 XX WPI; 1997-107141/10.
 XX Nucleic acid construct for gene expression - comprising DNA sequences
 PT encoding nuclear transport signal peptide and inducible repressor.
 XX Example 2; Col 43-50; 43pp; English.
 XX DNA constructs encoding a nuclear transport signal operatively linked to
 CC a DNA sequence encoding an inducible repressor are useful as vectors for
 CC expression of exogenous genes in eukaryotic cells in vitro and in vivo,
 CC e.g. for production of transgenic animals as models for human diseases.
 CC The present sequence is that of a luciferase reporter expression vector,
 CC pRSLuc. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 7223 BP; 1880 A; 1730 C; 1864 G; 1745 T; 0 U; 4 Other;
 Query Match 93.6%; Score 247.2; DB 2; Length 7223;
 Best Local Similarity 98.5%; Pred. No. 5.3e-76;
 Matches 260; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTACCA 60
 DB 2365 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTAACGATGAGTACCA 2424
 QY 61 TGCTTACAGAGAGAGAAAAGCAGCGTCATGCGGATGGTGGAGTAAGTGTACGA 120
 DB 2425 TGCTTACAGAGAGAGAAAAGCAGCGTCATGCGGATGGTGGAGTAAGTGTACGA 2484
 QY 121 TCCTGCTTATTAGAGAGCAACAGACGCGTCTGACATGATTTGACGACGACCACTAAAT 180
 DB 2485 TCCTGCTTATTAGAGAGCAACAGACGCGTCTGACATGATTTGACGACGACCACTAAAT 2544
 QY 181 CCGCATTCGAGAGAT-ATTGTAATTAAAGTGCCTAGCTCGATACAAATAAGCCATTGAC 239
 DB 2545 CCGCATTCGAGAGATATTGTAATTAAAGTGCCTAGCTCGATACAAATAAGCCATTGAC 2604
 QY 240 CATTCCACCATTTGGTGTGCACT 263
 DB 2605 CATTCCACCATTTGGTGTGCACT 2628
 RESULT 53
 AAT71261
 ID AAT71261 standard; DNA; 565 BP.
 XX
 AC AAT71261;
 XX
 XX 30-MAR-1998 (first entry)
 XX Rous sarcoma virus v-src gene.
 XX Cognate transgene; v-src gene; lymphoma; cellular immunogen; cancer;
 KW self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
 KW colon carcinoma; immunotherapy; proto-oncogene; rous sarcoma virus; ss.
 XX
 OS Rous sarcoma virus.
 XX
 PN W09725660-A1.
 XX
 PD 24-JUL-1997.
 XX

PF 13-JAN-1997; 97WO-US000582.
 XX
 PR 19-JAN-1996; 96US-0010262P.
 XX
 PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.
 XX Halpern MS, England JM;
 XX WPI; 1997-384993/35.
 XX
 PT Proto-oncogene immunogen - used in vaccine for the prevention and
 PT treatment of cancer.
 XX
 PS Disclosure; Page 69; 81pp; English.
 XX
 CC This sequence represents the Rous sarcoma virus v-src cognate transgene
 CC (CTG). Deletion of amino acids 430-433 of the encoded protein renders the
 CC CTG non-transforming. This sequence can be used in the cellular immunogen
 CC of the invention. The cellular immunogen of the invention is for
 CC immunising against the product of a target proto-oncogene, over-
 CC expression of which is associated with cancer, comprises host cells
 CC transfected with a construct containing at least one transgene related to
 CC the proto-oncogene and driven by a strong promoter. The product of the
 CC transgene induces immunoreactivity to host self-determinants on the
 CC product of proto-oncogene. The cellular immunogens are used for
 CC protective vaccination against cancer (e.g. carcinoma of breast or colon,
 CC or various lymphomas) and for immunotherapy of cancer. Use of the
 CC immunogen eliminates the need to isolate immunogenic, HLA host-matched
 CC peptides. The method is not based on immune recognition of a determinant
 CC defined by a cancer-specific mutation and generates a systemic (anti-
 CC metastatic) response
 XX
 SQ Sequence 565 BP; 148 A; 114 C; 162 G; 141 T; 0 U; 0 Other;
 Query Match 92.7%; Score 244.8; DB 2; Length 565;
 Best Local Similarity 97.4%; Pred. No. 1.2e-75;
 Matches 261; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
 QY 1 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATG-----GTAACGATGAGTAC 55
 DB 233 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGCTTATGATGATGAGTAC 292
 QY 56 CAACATGCGCTTACAGAGAGAGAAAAGCAGCGTGCATGCCGATTCGTTGGAAGTAAGTGG 115
 DB 293 CAACATGCGCTTACAGAGAGAGAAAAGCAGCGTGCATGCCGATTCGTTGGAAGTAAGTGG 352
 QY 116 TACATGCGTCTTATGAGAGAGCAACAGCGGTCTGACATGATTTGGACGACCACT 175
 DB 353 TACATGCGTCTTATGAGAGAGCAACAGCGGTCTGACATGATTTGGACGACCACT 412
 QY 176 AAATTCCGATTCGAGAGATATTGTAATTAAAGTGCCTAGCTCGATACAAATAAGCCATT 235
 DB 413 GAATTCCGATTCGAGAGATATTGTAATTAAAGTGCCTAGCTCGATACAAATAAGCCATT 472
 QY 236 TGACCATTCACCAATTTGGTGTGCACT 263
 DB 473 TGACCATTCACCAATTTGGTGTGCACT 500
 RESULT 54
 AAZ60824
 ID AAZ60824 standard; DNA; 565 BP.
 XX
 AC AAZ60824;
 XX
 DT 16-MAY-2000 (first entry)
 XX
 DE Nucleotide sequence of a cognate transgene of v-src.
 XX Cognate transgene; CTG; tumorigenic; cellular immunogen; immunisation;
 KW proto-oncogene; malignancy; allogenic cell; vaccine; cancer; ss.
 XX
 OS Rat sarcoma virus.

XX WO200004927-A1.
 PN 03-FEB-2000.
 PD 08-JUL-1999; 99WO-US015594.
 PF 24-JUL-1998; 98US-0093965P.
 PS (UYAL-) UNIV ALLEGHNEY HEALTH SCI.
 PA (HALP/) HALPERN M. S.
 PA (ENGL/) ENGLAND J. M.
 XX Halpern MS, England JM;
 PI WPI; 2000-182543/16.
 DR Cellular immunogens comprising allogenic donor cells transfected with a
 PT construct comprising a proto-oncogene cognate, useful as cancer vaccines.
 XX
 PS Disclosure; Page 75-76; 77pp; English.
 CC The present sequence represents a cognate transgene (CTG) which is
 CC rendered non-tumorigenic by deletion of amino acids 9-155. The CTG is
 CC used in the course of the invention. The specification describes a
 CC cellular immunogen for immunizing a host against the effects of the
 CC product of a target proto-oncogene which is associated with a
 CC malignancy. The cellular immunogen comprises allogenic cells transfected
 CC with transgene construct comprising a transgene cognate to target proto-
 CC oncogene and a strong promoter. The cellular immunogen is useful for
 CC vaccinating a host against cancer by inserting the transgene construct
 CC into the body of the host for the expression of the transgene. The method
 CC of the invention is designed to target mutation-driven non-self
 CC determinants. The cellular immunogens induce reactivity for self-
 CC determinants in the over expressed product of tumour associated and over
 CC expressed proto-oncogenes
 XX
 SQ Sequence 565 BP; 148 A; 114 C; 162 G; 141 T; 0 U; 0 Other;
 Query Match 92.7%; Score 244.8; DB 3; Length 565;
 Best Local Similarity 97.4%; Pred. No. 1.2e-75;
 Matches 261; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
 Qy 1 AATGTAGTCTTATGCAATATCTTTGTAGTCTTGTGCAACATG-----GTAACGATGAGTTAG 55
 Db 233 AATGTAGTCTTATGCAATATCTTTGTAGTCTTGTGCAACATGCTTATGTAACGATGAGTTAG 292
 Qy 56 CACATGCGCTTACAGAGGAGAAAGACCGATGCGATGCGGATGCGGAGTAAGGTGG 115
 Db 293 CACATGCGCTTACAGAGGAGAAAGACCGATGCGGATGCGGAGTAAGGTGG 352
 Qy 116 TACGATCGTCCCTTATTAGGAAGCAACAGACGGGTCTGACATGATTGGACGACCAT 175
 Db 353 TACGATCGTCCCTTATTAGGAAGCAACAGACGGGTCTGACATGATTGGACGACCAT 412
 Qy 176 AATTCGCGATTCGAGAGATTTGTTTAAAGTCCCTAGCTCGATACAAATTAACGCGCAT 235
 Db 413 GAATTCGCGATTCGAGAGATTTGTTTAAAGTCCCTAGCTCGATACAAATTAACGCGCAT 472
 Qy 236 TGACCATTCACACATGTTGTCACCT 263
 Db 473 TGACCATTCACACATGTTGTCACCT 500
 RESULT 55
 AAD28311
 ID AAD28311 standard; DNA; 5130 BP.
 AC AAD28311;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE LSRNL vector.

XX Regulatory element; vector; erythropoietin; growth hormone; insulin;
 KW immunoglobulin; bone morphogenetic protein; interferon; interleukin;
 KW superoxide dismutase; T-cell receptor; surface membrane protein; MoMuLV;
 KW viral antigen; transport protein; addressin; regulatory protein; MoMuLV;
 KW moloney murine leukemia virus; chimeric; hepatitis B virus; ds.
 XX
 OS Hepatitis B virus.
 OS Moloney murine leukemia virus.
 OS Unidentified.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT LTR 1..589 /*tag= a /*note= "MoMuLV 5' LTR"
 FT misc_feature 659..897 /*tag= b /*note= "Retroviral packaging region"
 FT misc_feature 1034..1714 /*tag= c /*note= "Hepatitis B surface antigen"
 FT promoter 2279..2595 /*tag= d /*note= "RSV promoter"
 FT misc_feature 2951..3745 /*tag= e /*note= "Neomycin phosphotransferase gene"
 FT LTR 4537..5130 /*tag= f /*note= "MoMuLV 3' LTR"
 XX WO2000202783-A2.
 PD 10-JAN-2002.
 XX 29-JUN-2001; 2001WO-US020714.
 XX 03-JUL-2000; 2000US-0215851P.
 PA (GALA-) GALA DESIGN INC.
 XX Bleck GT;
 XX WPI; 2002-154749/20.
 DR Novel regulatory elements including nucleic acid encoding hybrid alpha-
 PT lactalbumin promoter or mutant RNA export element, for expressing one or
 PT more proteins e.g. antibodies, pharmaceutical proteins in host cells.
 XX
 PS Example 1; Fig 12; 151pp; English.
 XX The invention relates to novel regulatory elements and vectors for the
 CC expression of one or more proteins in a host cell. The invention further
 CC provides methods of indirectly detecting the expression of a protein of
 CC interest, comprising providing the host cell transfected with a vector
 CC encoding a polycistronic sequence comprising a signal protein and a
 CC desired protein operably linked by an internal ribosome entry site
 CC (IRES), and culturing the host cell under suitable conditions so that the
 CC signal protein and the desired protein is produced, where the presence of
 CC elements and vectors of the invention are useful for the expression of
 CC proteins of interest in a host cell. They are useful for producing an
 CC immunoglobulin (Ig), preferably secretory Ig. They are useful in the
 CC expression of one or more proteins such as erythropoietin, growth
 CC hormone, insulin, immunoglobulins, protein C, cytokines and their
 CC receptors, hormones, Von Willebrands factor, lung surfactant, serum
 CC albumins, DNase, vascular endothelial growth factor, receptors for
 CC hormones or growth factors, rheumatoid factors, nerve growth factors, CD
 CC proteins, osteoinductive factors, immunotoxins, bone morphogenetic
 CC protein, interferons, colony stimulating factors, interleukins,
 CC superoxide dismutase, T-cell receptors, surface membrane proteins, viral
 CC antigens, transport proteins, addressins, regulatory proteins,

CC antibodies, chimeric proteins and their fragments. The vectors are
 CC particularly useful for expressing G protein coupled receptors and other
 CC transmembrane proteins. The retroviral vectors are useful for expressing
 CC proteins in mammalian tissue culture host cells, including rat fibroblast
 CC cells, bovine kidney cells and human kidney cells. The present sequence
 CC is LSRNL vector used in the invention. The vector comprises the following
 CC elements: moloney murine leukemia virus (MoMuLV) 5' LTR, MoMuLV viral
 CC packaging signal, hepatitis B surface antigen; RSV promoter; neomycin
 CC phosphotransferase gene and 3' MoMuLV LTR

SQ Sequence 5130 BP; 1187 A; 1335 C; 1332 G; 1276 T; 0 U; 0 Other;

Query Match 87.9%; Score 232; DB 6; Length 5130;
 Best Local Similarity 97.0%; Pred. No. 1e-70;
 Matches 258; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGTTAAGTACGATGAGTACCA 60
 DB 2325 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGTTAAGTACGATGAGTACCA 2384

QY 61 TGCCTTACAGGAGAGAAAAGACACCGCTGCATGCCGATTGGTGGAGTAAAGTGGTACGA 120
 DB 2385 TGCCTTACAGGAGAGAAAAGACACCGCTGCATGCCGATTGGTGGAGTAAAGTGGTACGA 2444

QY 121 TCGTGCCCTTATTAGGAGGCAACAGACCGGCTCTGACATGGAATGGACCACTAAAT 180
 DB 2445 TCGTGCCCTTATTAGGAGGCAACAGACAGGCTCTGACATGGAATGGACCACTAAAT 2504

QY 181 CCGCATTTGACAGAGAT-ATTGATTTAAGTGCTGCTAGCTGATACATTAACGCCA--TTTG 237
 DB 2505 CCGCATTTGACAGAGATTTATTATTAAAGTGCTGATACATTAACGCCA--TTTG 2564

QY 238 ACCATTACCAACATTTGGTGGCACT 263
 DB 2565 ACCATTACCAACATTTGGTGGCACT 2590

RESULT 56
 AAD28272

ID AAD28272 standard; DNA; 7170 BP.

XX AC AAD28272;

XX DT 22-APR-2002 (first entry)

XX DE LSRNL vector.

XX KW LSRNL vector; pharmaceutical; industrial; diagnostic; screening; MoMuLV;
 KW moloney murine leukemia virus; chimeric; hepatitis B virus; ds.

XX OS Hepatitis B virus.
 OS Moloney murine leukemia virus.
 OS Unidentified.
 OS Chimeric.

XX Key Location/Qualifiers

XX LTR 1..589
 /tag= a
 /note= "MoMuLV 5' LTR"

XX misc_feature 659..857
 /tag= b

XX misc_feature 1034..1714
 /note= "retroviral packaging region"

XX promoter 2279..2595
 /note= "Hepatitis B surface antigen"

XX misc_feature 2951..3745
 /note= "RSV promoter"

XX LTR 4537..5130
 /tag= e
 /note= "Neomycin phosphotransferase gene"

FT /note= "MoMuLV 3' LTR"

XX W0200202738-A2.

XX 10-JAN-2002.

XX 29-JUN-2001; 2001WO-US020710.

XX 03-JUL-2000; 2000US-0215925P.

XX (GALA-) GALA DESIGN INC.

XX Bremel RD, Millier LU, Black GT, York D;

XX WPI; 2002-154737/20.

XX Host cell for producing a desired protein and for screening compounds
 FT useful for pharmaceutical, industrial, diagnostic and other purposes,
 FT comprises multiple integrating vectors having an exogenous gene.

XX Example 1; Fig 12; 191pp; English.

XX The invention relates to a host cell comprising a genome having at least
 CC two integrated integrating vectors. The integrating vectors comprise at
 CC least one exogenous gene operably linked to a promoter. The host cell is
 CC useful for producing a desired protein and for comparing protein
 CC functions. The host cell comprises a reporter gene which is from gene
 CC fluorescent protein, luciferase, beta-galactosidase and beta-lactamase,
 CC and the assaying step further comprises detecting a signal from the
 CC reporter gene. The desired protein includes proteins for pharmaceutical,
 CC industrial, diagnostic and other purposes. The host cells is useful for
 CC indirectly detecting the expression of a desired protein, comprising
 CC providing the host cell transfected with a vector encoding a
 CC polycistronic sequence comprising a signal protein and a desired protein
 CC operably linked by an internal ribosome entry site (IRES), and culturing
 CC the host cell under suitable conditions so that the signal protein and
 CC the desired protein is produced, where the presence of signal protein
 CC indicates the presence of desired protein. The present sequence is LSRNL
 CC vector used in the invention. The vector comprises the following
 CC elements: moloney murine leukemia virus (MoMuLV) 5' LTR, MoMuLV viral
 CC packaging signal, hepatitis B surface antigen; RSV promoter; neomycin
 CC phosphotransferase gene and 3' MoMuLV LTR

XX SQ Sequence 7170 BP; 1688 A; 1891 C; 1841 G; 1750 T; 0 U; 0 Other;

Query Match 87.9%; Score 232; DB 6; Length 7170;
 Best Local Similarity 97.0%; Pred. No. 1.2e-70;
 Matches 258; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGTTAAGTACGATGAGTACCA 60
 DB 4365 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGCAATGTTAAGTACGATGAGTACCA 4424

QY 61 TGCCTTACAGGAGAGAAAAGACACCGCTGCATGCCGATTGGTGGAGTAAAGTGGTACGA 120
 DB 4425 TGCCTTACAGGAGAGAAAAGACACCGCTGCATGCCGATTGGTGGAGTAAAGTGGTACGA 4484

QY 121 TCGTGCCCTTATTAGGAGGCAACAGACCGGCTCTGACATGGAATGGACCACTAAAT 180
 DB 4485 TCGTGCCCTTATTAGGAGGCAACAGACAGGCTCTGACATGGAATGGACCACTAAAT 4544

QY 181 CCGCATTTGACAGAGAT-ATTGATTTAAGTGCTGCTAGCTGATACATTAACGCCA--TTTG 237
 DB 4545 CCGCATTTGACAGAGATTTATTATTAAAGTGCTGATACATTAACGCCA--TTTG 4604

QY 238 ACCATTACCAACATTTGGTGGCACT 263
 DB 4605 ACCATTACCAACATTTGGTGGCACT 4630

RESULT 57
 ACD27899

ID ACD27899 standard; DNA; 10468 BP.

XX ACD27899;
 XX
 XX 25-SEP-2003 (first entry)
 XX
 XX pdmT2 vector DNA sequence useful as a lentiviral vector.
 XX
 XX Lentiviral vector; transcriptional regulatory sequence; endothelial cell;
 KW VSV glycoprotein envelope; gene delivery; angiogenesis related pathology;
 KW vesicular stomatitis virus; selective gene expression; tissue ischemia;
 KW gene therapy; retinal neovascularisation; chronic inflammatory disorder;
 KW tumour; metastasis; cytostatic; antiinflammatory; vasotropic; pdmT2;
 KW lentivirus; human cytomegalovirus; hCMV; mouse; human; mutant; ds.
 XX
 XX Lentivirus sp.
 OS Mus sp.
 OS Homo sapiens.
 OS Human cytomegalovirus.
 OS Synthetic.
 XX US2003095948-A1.
 XX
 XX 22-MAY-2003.
 XX
 XX 28-MAY-2002; 2002US-00155736.
 XX
 XX 29-MAY-2001; 2001IT-MI001138.
 XX
 XX (UYTO-) UNIV TORINO.
 XX
 XX Maldini L, Palma MD;
 PI
 XX MPI; 2003-558321/52.
 XX
 XX New lentiviral vector construct for transferring nucleotide sequences in
 PT vivo and ex vivo, useful for treating tissue ischemia, retinal
 PT neovascularization, chronic inflammatory disorders, tumor or metastasis.
 XX
 XX Example; Fig 9A-9D; 21pp; English.
 XX
 XX The present invention relates to a lentiviral vector construct for
 CC transferring nucleotide sequences in vivo and ex vivo. The vector
 CC comprises transcriptional regulatory sequences of one or more genes
 CC preferentially expressed in the endothelial cells of mammals. The
 CC lentiviral vector also comprises a vesicular stomatitis virus (VSV)
 CC glycoprotein envelope that transduces the transfer of the vector
 CC construct. The lentiviral vector is useful for treating an angiogenesis
 CC related pathology by gene delivery and selective expression of a gene in
 CC cells engaged in angiogenesis. The lentiviral vector construct is useful
 CC for treating tissue ischemia, retinal neovascularisation, chronic
 CC inflammatory disorders, tumors or metastasis. The present sequence
 CC represents pdmT2 vector which may be used as a lentiviral vector
 XX
 XX SQ Sequence 10468 BP; 2764 A; 2437 C; 2638 G; 2629 T; 0 U; 0 Other;
 Query Match 82.3%; Score 217.4; DB 8; Length 10468;
 Best Local Similarity 99.1%; Pred. No. 2e-65;
 Matches 229; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 AATGTAGCTTATGCAATACTCTGTAGTCTTGTGCAATGTAAGTGGTACGA 60
 DB 2217 AATGTAGCTTATGCAATACTCTGTAGTCTTGTGCAATGTAAGTGGTACGA 2276
 QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGATGCCGATTTGGTGGAGTAAAGTGGTACGA 120
 DB 2277 TGCCTTACAAGGAGAGAAAAGCACCCTGATGCCGATTTGGTGGAGTAAAGTGGTACGA 2336
 QY 121 TCGTGGCTTATAGGAGGCAACAGACGGGTCTGATGATGATGACCAACCAATAATT 180
 DB 2337 TCGTGGCTTATAGGAGGCAACAGACGGGTCTGATGATGATGACCAACCAATAATT 2396
 QY 181 -CCGATTCGAGAGATATTGTATTAAAGTGCCTAGCTGATACATAACG 230

Db 2397 GCCGATTGCAGAGATATTGTATTAAAGTGCCTAGCTGATACATAAAGC 2447
 RESULT 58
 AAQ06310
 ID AAQ06310 standard; DNA; 3188 BP.
 XX
 XX AC AAQ06310;
 XX
 XX 25-MAR-2003 (revised)
 DT 29-JAN-1991 (first entry)
 XX
 XX Sequence of plasmid p79DBAM.
 XX
 XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
 KW hypersensitivity; ds.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT LTR 279..335
 FT /*tag= a
 FT polyA_signal 497..502
 FT /*tag= b
 XX
 XX BP393502-A.
 XX
 XX 24-OCT-1990.
 XX
 XX 11-APR-1990; 90EP-00106992.
 XX
 XX 19-APR-1989; 89EP-00810295.
 XX
 XX (HOFF) HOFFMANN-LA ROCHE AG.
 XX
 XX Fountoulak M, Garotta G, Stuber D;
 PI
 XX MPI; 1990-322042/43.
 XX
 XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
 PT chronic inflammations, etc.
 XX
 XX Disclosure; Fig 49; 174pp; English.
 XX
 XX IFN-gamma is a therapeutically active agent in the treatment of
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
 CC chronic inflammations and delayed hypersensitivity. It is also useful in
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 XX SQ Sequence 3188 BP; 797 A; 774 C; 882 G; 735 T; 0 U; 0 Other;
 Query Match 80.7%; Score 213; DB 2; Length 3188;
 Best Local Similarity 92.2%; Pred. No. 4.1e-64;
 Matches 248; Conservative 0; Mismatches 15; Indels 5; Gaps 2;
 QY 1 AATGTAGCTTATGCAATACTCTGTAGTCTTGTGCAATG-----GTAAAGTGGTAG 55
 DB 45 AATGTAGCTTATGCAATACTCTGTAGTCTTGTGCAATGCTTATGTAAGTGGTAG 104
 QY 56 CAATATGCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTGGAGTAAAGTGG 115
 DB 105 CAATATGCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTGGAGTAAAGTGG 164
 QY 116 TACGATGTCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGGACCAACT 175
 DB 165 TA-GATGTCCTTATTAGGAAGCAACAGACGGGTCTGACATGGATTGGACCAACT 223
 QY 176 AAATTCGCGATTCGAGAGATATTGTATTAAAGTGCCTAGCTGATACATAAAGCCATT 235
 DB 224 GAATTCGATTCGAGAGATATTGTATTAAAGTGCCTAGCTGATACATAAAGCCATT 283
 QY 236 TGACCATTCACACATTGGTGTGACCTC 264

Db 284 TGACCATTCACACATTGGTGTGCACCTC 312

RESULT 59
AAQ06311

ID AAQ06311 standard; DNA; 3276 BP.

XX AC AAQ06311;

XX 25-MAR-2003 (revised)

DT 29-JAN-1991 (first entry)

XX XX

DE Sequence of plasmid p238BGL.

XX XX

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;

KW hypersensitivity; ds.

XX XX

OS Homo sapiens.

XX XX

XX Key Location/Qualifiers

FT CDS 243..426

FT FT /*tag= b

FT FT 243..405

FT FT Sig-peptide

FT FT /*tag= c

FT FT /label= S.P.1

FT FT 279..242

FT FT /*tag= a

FT FT 585..590

FT FT /*tag= d

XX XX

XX ZP393502-A.

XX XX

XX 24-OCT-1990.

XX XX

XX 11-APR-1990; 90EP-00106992.

XX XX

XX 19-APR-1989; 89EP-00810295.

XX XX

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX XX

XX Fountoulak M, Garotta G, Stuber D;

XX XX

XX WPI; 1990-322042/43.

DR P-PSDB; AAR07065.

XX XX

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,

XX XX

XX chronic inflammations, etc.

XX XX

XX Disclosure; Fig 51; 174pp; English.

XX XX

XX IFN-gamma is a therapeutically active agent in the treatment of

CC autoimmune disease, allograft transplant rejections, multiple sclerosis,

CC chronic inflammations and delayed hypersensitivity. It is also useful in

CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.

CC (updated on 25-MAR-2003 to correct PR field.)

XX XX

XX Sequence 3276 BP; 814 A; 794 C; 914 G; 754 T; 0 U; 0 Other;

XX XX

Query Match 80.7%; Score 213; DB 2; Length 3276;

Best Local Similarity 92.2%; Pred. No. 4.2e-64;

Matches 248; Conservative 0; Mismatches 15; Indels 6; Gaps 2;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATG-----GTAACGATGAGTTAG 55

Db 45 AATGTAGCTTATGCATATCTTGTAGTCTTGCACATGCTTATGTACGATGAGTTAG 104

QY 56 CAACATGCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGGTGGAGTAAGTTGG 115

Db 105 CAACATGCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGGTGGAGTAAGTTGG 164

QY 116 TACATCGTGCCTTATTAGAGAGCAACACACGGGTCTGACATGATTTGGAGTAAGTGG 175

Db 165 TA-GATCGTGCCTTATTAGAGAGCAACACACGGGTCTGACATGATTTGGAGTAAGTGG 22

QY 176 AAATTCGCGCATTCGAGATATTTGTTAAAGTGCTAGCTCGATACAATAAAGCCATT 235

Db 224 GAATTCGCATTGCAGAGAGTATTGTATTAAAGTGCTAGCTCGATACAATAAAGCCATT 283

QY 236 TGACCATTCACACATTGGTGTGCACCTC 264

Db 284 TGACCATTCACACATTGGTGTGCACCTC 312

RESULT 60
AAQ06309

ID AAQ06309 standard; DNA; 3383 BP.

XX AC AAQ06309;

XX 25-MAR-2003 (revised)

DT 29-JAN-1991 (first entry)

XX XX

DE Sequence of plasmid p76BGL.

XX XX

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;

KW hypersensitivity; ds.

XX XX

OS Homo sapiens.

XX XX

XX Key Location/Qualifiers

FT LTR 279..504

FT FT /*tag= a

FT CDS 505..540

FT FT /*tag= b

FT polyA_signal

FT 692..697

FT FT /*tag= c

XX XX

XX EP393502-A.

XX XX

XX 24-OCT-1990.

XX XX

XX 11-APR-1990; 90EP-00106992.

XX XX

XX 19-APR-1989; 89EP-00810295.

XX XX

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX XX

XX Fountoulak M, Garotta G, Stuber D;

XX XX

XX WPI; 1990-322042/43.

DR P-PSDB; AAR07065.

XX XX

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,

XX XX

XX chronic inflammations, etc.

XX XX

XX Disclosure; Fig 47; 174pp; English.

XX XX

XX IFN-gamma is a therapeutically active agent in the treatment of

CC autoimmune disease, allograft transplant rejections, multiple sclerosis,

CC chronic inflammations and delayed hypersensitivity. It is also useful in

CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.

CC (updated on 25-MAR-2003 to correct PR field.)

XX XX

XX Sequence 3383 BP; 838 A; 828 C; 929 G; 788 T; 0 U; 0 Other;

XX XX

Query Match 80.7%; Score 213; DB 2; Length 3383;

Best Local Similarity 92.2%; Pred. No. 4.3e-64;

Matches 248; Conservative 0; Mismatches 15; Indels 6; Gaps 2;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATG-----GTAACGATGAGTTAG 55

Db 45 AATGTAGCTTATGCATATCTTGTAGTCTTGCACATGCTTATGTACGATGAGTTAG 104

QY 56 CAACATGCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGGTGGAGTAAGTGG 115

Db 105 CAACATGCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGGTGGAGTAAGTGG 164

QY 116 TACATCGTGCCTTATTAGAGAGCAACACACGGGTCTGACATGATTTGGAGTAAGTGG 175

Db 284 TGACCATTCACACATTGGTGTGCACCTC 312

RESULT 59
AAQ06311

ID AAQ06311 standard; DNA; 3276 BP.

XX AC AAQ06311;

XX 25-MAR-2003 (revised)

DT 29-JAN-1991 (first entry)

XX XX

DE Sequence of plasmid p238BGL.

XX XX

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;

KW hypersensitivity; ds.

XX XX

OS Homo sapiens.

XX XX

XX Key Location/Qualifiers

FT CDS 243..426

FT FT /*tag= b

FT FT 243..405

FT FT Sig-peptide

FT FT /*tag= c

FT FT /label= S.P.1

FT FT 279..242

FT FT /*tag= a

FT FT 585..590

FT FT /*tag= d

XX XX

XX ZP393502-A.

XX XX

XX 24-OCT-1990.

XX XX

XX 11-APR-1990; 90EP-00106992.

XX XX

XX 19-APR-1989; 89EP-00810295.

XX XX

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX XX

XX Fountoulak M, Garotta G, Stuber D;

XX XX

XX WPI; 1990-322042/43.

DR P-PSDB; AAR07065.

XX XX

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,

XX XX

XX chronic inflammations, etc.

XX XX

XX Disclosure; Fig 51; 174pp; English.

XX XX

XX IFN-gamma is a therapeutically active agent in the treatment of

CC autoimmune disease, allograft transplant rejections, multiple sclerosis,

CC chronic inflammations and delayed hypersensitivity. It is also useful in

CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.

CC (updated on 25-MAR-2003 to correct PR field.)

XX XX

XX Sequence 3276 BP; 814 A; 794 C; 914 G; 754 T; 0 U; 0 Other;

XX XX

Query Match 80.7%; Score 213; DB 2; Length 3276;

Best Local Similarity 92.2%; Pred. No. 4.2e-64;

Matches 248; Conservative 0; Mismatches 15; Indels 6; Gaps 2;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATG-----GTAACGATGAGTTAG 55

Db 45 AATGTAGCTTATGCATATCTTGTAGTCTTGCACATGCTTATGTACGATGAGTTAG 104

QY 56 CAACATGCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGGTGGAGTAAGTTGG 115

Db 105 CAACATGCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGGTGGAGTAAGTTGG 164

QY 116 TACATCGTGCCTTATTAGAGAGCAACACCGGGTCTGACATGATTTGGAGTAAGTGG 175

Db 165 TA-GATGTGCTTATTAGGAAGCAACAGACGGGTCTGACATGATTCGAGAACACCC 22

QY 176 AAATTCGCAATTCGAGATATTTGTTAAAGTGCTAGCTCGATACAATAAAGCCATT 235

Db 224 GAATTCGCAATTCGAGAGATTTGTTATTAAAGTGCTAGCTCGATACAATAAAGCCATT 283

QY 236 TGACCATTCACCACTTGGTGTGCACCTC 264

Db 284 TGACCATTCACCACTTGGTGTGCACCTC 312

RESULT 60
AAQ06309

ID AAQ06309 standard; DNA; 3383 BP.

XX AC AAQ06309;

XX 25-MAR-2003 (revised)

DT 29-JAN-1991 (first entry)

XX XX

DE Sequence of plasmid p76BGL.

XX XX

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;

KW hypersensitivity; ds.

XX XX

OS Homo sapiens.

XX XX

XX Key Location/Qualifiers

FT LTR 279..504

FT FT /*tag= a

FT CDS 505..540

FT FT /*tag= b

FT FT polyA_signal

FT FT 692..697

FT FT /*tag= c

XX XX

XX EP393502-A.

XX XX

XX 24-OCT-1990.

XX XX

XX 11-APR-1990; 90EP-00106992.

XX XX

XX 19-APR-1989; 89EP-00810295.

XX XX

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX XX

XX Fountoulak M, Garotta G, Stuber D;

XX XX

XX WPI; 1990-322042/43.

DR P-PSDB; AAR07065.

XX XX

XX Soluble interferon-gamma receptors - for treating auto-immune diseases,

XX XX

XX chronic inflammations, etc.

XX XX

XX Disclosure; Fig 47; 174pp; English.

XX XX

XX IFN-gamma is a therapeutically active agent in the treatment of

CC autoimmune disease, allograft transplant rejections, multiple sclerosis,

CC chronic inflammations and delayed hypersensitivity. It is also useful in

CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.

CC (updated on 25-MAR-2003 to correct PR field.)

XX XX

XX Sequence 3383 BP; 838 A; 828 C; 929 G; 788 T; 0 U; 0 Other;

XX XX

Query Match 80.7%; Score 213; DB 2; Length 3383;

Best Local Similarity 92.2%; Pred. No. 4.3e-64;

Matches 248; Conservative 0; Mismatches 15; Indels 6; Gaps 2;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATG-----GTAACGATGAGTTAG 55

Db 45 AATGTAGCTTATGCATATCTTGTAGTCTTGCACATGCTTATGTACGATGAGTTAG 104

QY 56 CAACATGCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGGTGGAGTAAGTGG 115

Db 105 CAACATGCTTACAGGAGAGAAAAGCACCGTGATGCCGATTGGTGGAGTAAGTGG 164

QY 116 TACATCGTGCCTTATTAGAGAGCAACACCGGGTCTGACATGATTTGGAGTAAGTGG 175

Db 105 CAACATGCTTACAGAGAGAGAAAAGACCGCTGATGCCGATTGGTGGAGTAAGGTGG 164
 QY 116 TACGATCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACACT 175
 Db 165 TA-GATCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACACT 223
 QY 176 AAATTCGGCATTCGAGAGATATTGTTTAAAGTGCCTAGCTCGATACAAATAAAGCCATT 235
 Db 224 GAATTCGCATTGCAGAGAGATATTGTTTAAAGTGCCTAGCTCGATACAAATAAAGCCATT 283
 QY 236 TGACCATTCACCAATTCGGTGCACCTC 264
 Db 284 TGACCATTCACCAATTCGGTGCACCTC 312

RESULT 61
 AAQ06313
 ID AAQ06313 standard; DNA; 3427 BP.
 XX AC AAQ06313;
 XX DT 25-MAR-2003 (revised)
 XX DT 29-JAN-1991 (first entry)
 XX DE Sequence of plasmid p267BGL.
 XX KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;
 XX KW hypersensitivity; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT LTR 279..492
 XX FT /*tag= a
 XX FT CDS 493..585
 XX FT /*tag= b
 XX FT Sig-peptide 493..564
 XX FT /*tag= c
 XX FT /*label= S.P.2
 XX FT polyA_signal 736..741
 XX FT /*tag= d
 XX EN EF393502-A.
 XX PD 24-OCT-1990.
 XX PF 11-APR-1990; 90EP-00106992.
 XX PR 19-APR-1989; 89EP-00810295.
 XX PA (HOFF) HOFFMANN-LA ROCHE AG.
 XX PI Fountoulak M, Garotta G, Stuber D;
 XX WPI; 1990-322042/43.
 XX P-PSDB; AAR07067.
 XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
 XX chronic inflammations, etc.
 XX PS Disclosure; Fig 59; 174pp; English.
 XX CC IFN-gamma is a therapeutically active agent in the treatment of
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
 CC chronic inflammations and delayed hypersensitivity. It is also useful in
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.
 XX (Updated on 25-MAR-2003 to correct PR field.)
 XX SQ Sequence 3427 BP; 846 A; 840 C; 942 G; 799 T; 0 U; 0 Other;
 Query Match 80.7%; Score 213; DB 2; Length 3427;
 Best Local Similarity 92.2%; Pred. No. 4.3e-64;
 Matches 248; Conservative 0; Mismatches 15; Indels 6; Gaps 2;

QY 1 AATGATGCTTATGCAATCTCTTGTAGTCTTTGCACATG-----CTAACGATGAGTTAG 55
 Db 45 AATGATGCTTATGCAATCTCTTGTAGTCTTTGCACATGCTTATGTAACGATGAGTTAG 104
 QY 56 CAACATGCTTACAGAGAGAGAAAAGACCGCTGATGCCGATTGGTGGAGTAAGGTGG 115
 Db 105 CAACATGCTTACAGAGAGAGAAAAGACCGCTGATGCCGATTGGTGGAGTAAGGTGG 164
 QY 116 TACGATCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACACT 175
 Db 165 TA-GATCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGCATGATGATGGAGCAACACT 223
 QY 176 AAATTCGGCATTCGAGAGATATTGTTTAAAGTGCCTAGCTCGATACAAATAAAGCCATT 235
 Db 224 GAATTCGCATTGCAGAGAGATATTGTTTAAAGTGCCTAGCTCGATACAAATAAAGCCATT 283
 QY 236 TGACCATTCACCAATTCGGTGCACCTC 264
 Db 284 TGACCATTCACCAATTCGGTGCACCTC 312

RESULT 62
 AAQ06312
 ID AAQ06312 standard; DNA; 3979 BP.
 XX AC AAQ06312;
 XX DT 25-MAR-2003 (revised)
 XX DT 29-JAN-1991 (first entry)
 XX DE Sequence of plasmid p264BGL.
 XX KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;
 XX KW hypersensitivity; ds.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT CDS 243..426
 XX FT /*tag= b
 XX FT Sig-peptide 243..405
 XX FT /*tag= c
 XX FT /*label= S.P.1
 XX FT LTR 279..242
 XX FT /*tag= a
 XX FT polyA_signal 1288..1292
 XX FT /*tag= d
 XX EN EF393502-A.
 XX PD 24-OCT-1990.
 XX PF 11-APR-1990; 90EP-00106992.
 XX PR 19-APR-1989; 89EP-00810295.
 XX PA (HOFF) HOFFMANN-LA ROCHE AG.
 XX PI Fountoulak M, Garotta G, Stuber D;
 XX WPI; 1990-322042/43.
 XX P-PSDB; AAR07066.
 XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
 XX chronic inflammations, etc.
 XX PS Disclosure; Fig 55; 174pp; English.
 XX CC IFN-gamma is a therapeutically active agent in the treatment of
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
 CC chronic inflammations and delayed hypersensitivity. It is also useful in
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.

CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
 CC which may be useful as therapeutic agents or therapeutic targets, e.g.
 CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
 CC proliferation or metabolic processes etc. The protein can also be used to
 CC screen for specific modulators. The nucleic acid can also be used as
 CC sources of therapeutic antisense or ribozyme sequences. The method allows
 CC the protein (rather than a partial DNA sequence) to be isolated and
 CC since a wide range of cells can be used, they can be expressed with the
 CC correct glycosylation pattern

SX Sequence 9542 BP; 2463 A; 2516 C; 2387 G; 2176 T; 0 U; 0 Other;
 Query Match 77.7%; Score 205.2; DB 2; Length 9542;
 Best Local Similarity 98.6%; Pred. No. 3.7e-61;
 Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACAT 61
 DB 665 ATCCAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACAT 724
 QY 62 GCCTTACAGGAGAGAAAAGCACCCTGATGCCGATGGTGGAGTAAGTGTACGAT 121
 DB 725 GCCTTACAGGAGAGAAAAGCACCCTGATGCCGATGGTGGAGTAAGTGTACGAT 784
 QY 122 CGTGCCTTATAGGAGGCAACAGACGCGGTCTGCATGATGGAGTGGACCACTAAATTC 181
 DB 785 CGTGCCTTATAGGAGGCAACAGACGCGGTCTGCATGATGGAGTGGACCACTAAATTC 844
 QY 182 CGCATTTGCAGAGATATTGTATTAAAGTGCC 211
 DB 845 CGCATTTGCAGAGATATTGTATTAAAGTGCC 874

RESULT 65
 AA90391
 ID AAA90391 standard; DNA; 9542 BP.
 AC AAA90391;
 DT 10-JAN-2001 (first entry)
 DE 987BNeo DNA sequence.
 KW Nucleic acid identification; exogenous protein; drug screening;
 KW recombinant expression; 987BNeo; ds.
 OS Synthetic.
 PN JP2000189173-A.
 PD 11-JUL-2000.
 PF 23-AUG-1999; 99JP-00236220.
 PR 17-NOV-1998; 98US-00193707.
 PR 17-NOV-1998; 98WO-US024520.
 XX (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
 XX WPI; 2000-551637/51.
 XX Identifying a recombinant nucleic acid to identify and isolate various
 PT cellular proteins, comprises culturing a composition comprising
 PT eukaryotic host cells and identifying a cell comprising recombinant
 PT nucleic acid.

XX Example 13; Fig 13A-C; 56pp; Japanese.
 XX The invention relates to the identification of a recombinant nucleic acid
 CC encoding an exogenous protein having a selected property. The method
 CC comprises preparing populations of eukaryotic host cells, where each cell
 CC comprises an expression vector encoding a different exogenous protein.
 CC The host cells are cultured under suitable conditions and the nucleic

CC acid which encodes the exogenous protein is identified. The method is
 CC useful for the identification and isolation of proteins with a selected
 CC property. Typical applications of the nucleic acid and the exogenous
 CC protein are in isolation of new growth factors, cytokines, membrane
 CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may
 CC be useful as therapeutic agents or therapeutic targets, e.g., pro-
 CC apoptotic or tumour suppressing proteins, regulators of cell
 CC proliferation or of metabolic processes. The protein can also be used to
 CC screen for ligands and specific modulators of activity. The method of the
 CC invention allows the direct cloning of full length cDNAs in one step. It
 CC facilitates direct expression of the protein without the need to perform
 CC further procedures such as subcloning and establishment of a cell line
 CC for protein production. The method allows a protein of interest (rather
 CC than a partial DNA sequence) to be isolated and, since a wide range of
 CC cell types can be used, they can be expressed in a correctly folded and
 CC glycosylated form. The present sequence represents the DNA sequence
 CC 987BNeo which was used in the exemplifications of the invention. This
 CC patent is related to WO9925876

SX Sequence 9542 BP; 2463 A; 2516 C; 2387 G; 2176 T; 0 U; 0 Other;
 Query Match 77.7%; Score 205.2; DB 3; Length 9542;
 Best Local Similarity 98.6%; Pred. No. 3.7e-61;
 Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACAT 61
 DB 665 ATCCAGTCTTATGCAATACCTCTTGTAGTCTTGGCAACATGTAACGATGAGTTAGCAACAT 724
 QY 62 GCCTTACAGGAGAGAAAAGCACCCTGATGCCGATGGTGGAGTAAGTGTACGAT 121
 DB 725 GCCTTACAGGAGAGAAAAGCACCCTGATGCCGATGGTGGAGTAAGTGTACGAT 784
 QY 122 CGTGCCTTATAGGAGGCAACAGACGCGGTCTGCATGATGGAGTGGACCACTAAATTC 181
 DB 785 CGTGCCTTATAGGAGGCAACAGACGCGGTCTGCATGATGGAGTGGACCACTAAATTC 844
 QY 182 CGCATTTGCAGAGATATTGTATTAAAGTGCC 211
 DB 845 CGCATTTGCAGAGATATTGTATTAAAGTGCC 874

RESULT 66
 AAZ27850
 ID AAZ27850 standard; cDNA; 11282 BP.
 AC AAZ27850;
 DT 23-DEC-1999 (first entry)
 DE Complete cDNA sequence of pCVTts.
 KW Gene expression system; cis-acting element; gene therapy;
 KW temperature-sensitive RNA-dependent RNA polymerase;
 KW inducible alphaviral gene expression system; pCVTts;
 KW hormone-based gene control system; tetracycline gene control system; ss.
 OS Synthetic.
 XX WO9950432-A1.
 XX 07-OCT-1999.
 XX 25-MAR-1999; 99WO-IB000523.
 XX 27-MAR-1998; 98US-0079562P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX (ZENN/) RENNER W A.
 XX (NIEB/) NIEBA L.
 XX (BOOR/) BOORSMA M.
 XX Renner WA, Nieba L, Boorsma M;
 PI

XX DR WPI; 1999-591327/50.
XX PT A new system to regulate gene expression in eukaryotic cells.
XX PS Claim 15; Fig 3; 99pp; English.
XX CC This sequence represents the complete cDNA sequence for the vector
CC pCytts. The invention relates to a DNA molecule comprising a
CC polynucleotide (I) encoding an RNA molecule. The encoded RNA comprises:
CC (a) at least one cis-acting element; (b) an open reading frame (ORF1)
CC encoding a non-cyclophatic, temperature-sensitive RNA-dependent RNA
CC polymerase; and (c) a second sequence that is: (i) a protein-encoding ORF
CC (ORF2) that is in a translatable format after RNA-dependent RNA
CC replication event(s); (ii) a sequence complementary to the ORF2; or (iii)
CC a sequence encoding an untranslated RNA molecule. The pCytts sequence is
CC an example of the DNA molecule, and is an inducible alphavirus gene
CC expression system. The invention is used in gene therapy and recombinant
CC technology to regulate expression of introduced genes. The invention does
CC not have the problems of toxicity and/or high basal level expression
CC associated with prior art tetracycline-based and hormone-based gene
CC control systems
XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;
Query Match 77.7%; Score 205.2; DB 2; Length 11282;
Best Local Similarity 98.6%; Pred. No. 4e-61;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 ATGAGCTCTTATGCAATACCTCTTTAGTCTTGGCAATGTTAGCAAGTGTAGCAACAT 61
Db 664 ATCCAGCTCTTATGCAATACCTCTTTAGTCTTGGCAATGTTAGCAAGTGTAGCAACAT 723
QY 62 GCCTTACAGAGGAG 121
Db 724 GCCTTACAGAGGAG 783
QY 122 CGTGCCTTATTAGGAGGAG 181
Db 784 CGTGCCTTATTAGGAGGAG 843
QY 182 CGCATTCGACAGATATTGTATTATTTAAGTCCC 211
Db 844 CGCATTCGACAGATATTGTATTATTTAAGTCCC 873
RESULT 67
AAD04741
ID AAD04741 standard; cDNA; 11282 BP.
XX AC AAD04741;
XX 17-JUL-2001 (first entry)
XX DE Alphaviral vector pCytts cDNA.
XX pCytts; alphaviral vector; vaccine; therapy; cancer; antiparasitic;
XX antimalarial; anticancer; anti-HIV; antiviral; infectious disease;
XX Human immunodeficiency virus; HIV; influenza; passive immunisation;
XX carcinoma; liver; skin; stomach; ovarian tumour; ss.
XX Rous sarcoma virus.
OS Alphavirus.
OS Unidentified.
OS Chimeric.
XX WO200130989-A2.
XX 03-MAY-2001.
XX 26-OCT-2000; 2000WO-1B001557.
XX 27-OCT-1999; 99US-016796P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX FA (RENN/) RENNER W A.
XX NIIEB/) NIEBA L.
XX Renner WA, Nieba L;
XX WPI; 2001-308631/32.
XX
XX Preparing alphaviral vectors with mutations in a selected gene, for use
XX as vaccines, particularly against pathogens that mutate rapidly,
XX comprises replicating in the presence of a nucleoside analog.
XX Claim 6; Fig 3; 103pp; English.
XX
XX The present invention relates to a method for preparing viral vectors
XX which comprises inserting a gene of interest into an alphaviral vector
XX such as pCytts, pinRep5 and replicating the vector in the presence of
XX alphaviral replicase and nucleoside analogues (5'azacytidine (AZT), FU-
XX 5' fluorouridine) to produce a modified gene of interest. The replication
XX is repeated until the modified gene in 90 % of the vector population
XX contain a mutation in the modified gene which is 90-99 % identical with
XX the gene of interest. The vector populations are used in vaccines for
XX treatment or prevention of a wide variety of infectious diseases (viral
XX or parasitic, e.g. human immuno deficiency virus (HIV), influenza,
XX Trypanosoma or plasmodium) and cancers such as liver carcinoma, stomach
XX carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the
XX mutant populations will therefore be effective against viral escape
XX mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins
XX are correctly glycosylated. Antisera raised against the vaccines can be
XX used for passive immunisation. The present cDNA sequence is an alphaviral
XX vector pCytts. The vector contains Rous Sarcoma Virus promoter, cis-
XX acting sequence elements, non-structural proteins 1-4, gene of interest,
XX alphavirus subgenomic promoter, ampicillin resistance marker for
XX selection and a CoIE1 sequence for bacterial amplification
XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;
Query Match 77.7%; Score 205.2; DB 4; Length 11282;
Best Local Similarity 98.6%; Pred. No. 4e-61;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 ATGAGCTCTTATGCAATACCTCTTTAGTCTTGGCAATGTTAGCAAGTGTAGCAACAT 61
Db 664 ATCCAGCTCTTATGCAATACCTCTTTAGTCTTGGCAATGTTAGCAAGTGTAGCAACAT 723
QY 62 GCCTTACAGAGGAG 121
Db 724 GCCTTACAGAGGAG 783
QY 122 CGTGCCTTATTAGGAGGAG 181
Db 784 CGTGCCTTATTAGGAGGAG 843
QY 182 CGCATTCGACAGATATTGTATTATTTAAGTCCC 211
Db 844 CGCATTCGACAGATATTGTATTATTTAAGTCCC 873
RESULT 68
AAF84024
ID AAF84024 standard; cDNA; 11282 BP.
XX AC AAF84024;
XX 22-AUG-2001 (first entry)
XX Complete cDNA sequence of plasmid pCytts.
XX pCytts; cellular; taxol; gene therapy; RNA replication; endogenous gene;
XX ss.
XX Synthetic.


```
XX AC AAD53272;
XX XX
XX DT 28-MAY-2003 (first entry)
XX DE MESV2/EGFP/RSV retroviral vector DNA.
XX KW Retroviral vector; congenital disease; cancer; Parkinson's disease;
XX KW Alzheimer's disease; gene therapy; retroviral DNA; ds.
XX OS Retrovirus.
XX PN WO200294989-A2.
XX PD 28-NOV-2002.
XX PF 17-MAY-2002; 2002WO-US015816.
XX PR 18-MAY-2001; 2001US-0292201P.
XX PR 30-NOV-2001; 2001US-0334972P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Edelman GM, Owens G;
XX XX
XX DR WPI; 2003-140366/13.
XX PT New retroviral vector plasmid for introducing expressible polynucleotides
XX PT into cells, comprises a retrovirus long terminal repeat having U5, R and
XX PT U3 regions, a constitutive transport element, and a cloning site.
XX PS Claim 18; Col 95-97; 61pp; English.
XX CC The invention relates to novel retroviral vector plasmids for introducing
XX CC expressible polynucleotides into cells. The vectors comprise a retrovirus
XX CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive
XX CC transport element (CRE) and a cloning site. The retroviral vector plasmid
XX CC is useful in introducing an expressible polynucleotide into a cell such
XX CC as a neural stem cell and in treating or ameliorating a pathologic
XX CC condition in a subject such as a congenital diseases, cancer, Parkinson's
XX CC disease or Alzheimer's disease. The plasmid may also be used to produce
XX CC retroviral vectors useful for delivering genes into eukaryotic cells in
XX CC culture and in living organisms. Sequences of the invention are also
XX CC useful in gene therapy. The present sequence is MESV2/EGFP/RSV retroviral
XX CC vector DNA
XX SQ Sequence 4993 BP; 1206 A; 1328 C; 1303 G; 1156 T; 0 U; 0 Other;

Query Match 66.0%; Score 174.2; DB 7; Length 4993;
Best Local Similarity 98.3%; Pred. No. 2.4e-50;
Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGTTGCAATGTTAGCAACA 60
Db 1908 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGTTGCAATGTTAGCAACA 1967

QY 61 TGCCTTACAGGAGAGAAAAGCAGCGGTGTCATGCGGATTTGGGAAGTAAAGTGGTAGCA 120
Db 1968 TGCCTTACAGGAGAGAAAAGCAGCGGTGTCATGCGGATTTGGGAAGTAAAGTGGTAGCA 2027

QY 121 TCGTGCCTTATTAGAGGCAACAGACGGGTCTGACATGGATTGGACCAACCACTAAAT 179
Db 2028 TCGTGCCTTATTAGAGGCAACAGACGGGTCTGACATGGATTGGACCAACCACTAGAT 2086

RESULT 71
AAD53270
ID AAD53270 standard; DNA; 5643 BP.
XX AC AAD53270;
XX XX
XX DT 28-MAY-2003 (first entry)
XX XX
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DE MESV/ACTE/IRESEGFP retroviral vector DNA.
XX XX
XX KW Retroviral vector; congenital disease; cancer; Parkinson's disease;
XX KW Alzheimer's disease; gene therapy; retroviral DNA; ds.
XX OS Retrovirus.
XX PN WO200294989-A2.
XX PD 28-NOV-2002.
XX PF 17-MAY-2002; 2002WO-US015816.
XX PR 18-MAY-2001; 2001US-0292201P.
XX PR 30-NOV-2001; 2001US-0334972P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Edelman GM, Owens G;
XX XX
XX DR WPI; 2003-140366/13.
XX PT New retroviral vector plasmid for introducing expressible polynucleotides
XX PT into cells, comprises a retrovirus long terminal repeat having U5, R and
XX PT U3 regions, a constitutive transport element, and a cloning site.
XX PS Claim 18; Col 98-91; 61pp; English.
XX CC The invention relates to novel retroviral vector plasmids for introducing
XX CC expressible polynucleotides into cells. The vectors comprise a retrovirus
XX CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive
XX CC transport element (CRE) and a cloning site. The retroviral vector plasmid
XX CC is useful in introducing an expressible polynucleotide into a cell such
XX CC as a neural stem cell and in treating or ameliorating a pathologic
XX CC condition in a subject such as a congenital diseases, cancer, Parkinson's
XX CC disease or Alzheimer's disease. The plasmid may also be used to produce
XX CC retroviral vectors useful for delivering genes into eukaryotic cells in
XX CC culture and in living organisms. Sequences of the invention are also
XX CC useful in gene therapy. The present sequence is MESV/ACTE/IRESEGFP
XX CC retroviral vector DNA
XX SQ Sequence 5643 BP; 1356 A; 1505 C; 1472 G; 1310 T; 0 U; 0 Other;

Query Match 66.0%; Score 174.2; DB 7; Length 5643;
Best Local Similarity 98.3%; Pred. No. 2.5e-50;
Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGTTGCAATGTTAGCAACA 60
Db 2558 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGTTGCAATGTTAGCAACA 2617

QY 61 TGCCTTACAGGAGAGAAAAGCAGCGGTGTCATGCGGATTTGGGAAGTAAAGTGGTAGCA 120
Db 2618 TGCCTTACAGGAGAGAAAAGCAGCGGTGTCATGCGGATTTGGGAAGTAAAGTGGTAGCA 2677

QY 121 TCGTGCCTTATTAGAGGCAACAGACGGGTCTGACATGGATTGGACCAACCACTAAAT 179
Db 2678 TCGTGCCTTATTAGAGGCAACAGACGGGTCTGACATGGATTGGACCAACCACTAGAT 2736

RESULT 72
AAD53271
ID AAD53271 standard; DNA; 5643 BP.
XX AC AAD53271;
XX XX
XX DT 28-MAY-2003 (first entry)
XX XX
XX DE MESV2/IRESEGFP/RSV retroviral vector DNA.
XX KW Retroviral vector; congenital disease; cancer; Parkinson's disease;
XX KW Alzheimer's disease; gene therapy; retroviral DNA; ds.
XX XX
```


OS Retrovirus.
 XX WO200294989-A2.
 XX
 XX 28-NOV-2002.
 XX
 XX 17-MAY-2002; 2002WO-US015816.
 XX
 XX 18-MAY-2001; 2001US-0292201P.
 PR 30-NOV-2001; 2001US-0334972P.
 XX (Scri) SCRIPPS RES INST.
 XX Edelman GM, Owens G;
 XX WPI; 2003-140366/13.
 XX
 XX New retroviral vector plasmid for introducing expressible polynucleotides
 PT into cells, comprises a retrovirus long terminal repeat having U5, R and
 PT U3 regions, a constitutive transport element, and a cloning site.
 PT
 XX Claim 18; Col 91-94; 61pp; English.
 XX
 XX The invention relates to novel retroviral vector plasmids for introducing
 CC expressible polynucleotides into cells. The vectors comprise a retrovirus
 CC long terminal repeat (LTR) having U5, R and U3 regions, a constitutive
 CC transport element (CTE) and a cloning site. The retroviral vector plasmid
 CC is useful in introducing an expressible polynucleotide into a cell such
 CC as a neural stem cell and in treating or ameliorating a pathologic
 CC condition in a subject such as a congenital diseases, cancer, Parkinson's
 CC disease or Alzheimer's disease. The plasmid may also be used to produce
 CC retroviral vectors useful for delivering genes into eukaryotic cells in
 CC culture and in living organisms. Sequences of the invention are also
 CC useful in gene therapy. The present sequence is MESV2/IRESEGFP/RSV
 CC retroviral vector DNA
 XX
 XX Sequence 5643 BP; 1356 A; 1506 C; 1472 G; 1309 T; 0 U; 0 Other;
 SQ
 Query Match 66.0%; Score 174.2; DB 7; Length 5643;
 Best Local Similarity 98.3%; Pred. No. 2.5e-50;
 Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATATCTTTGAGTCTTGTGCAATGTTGCAATGTTAGTACCA 60
 Db 2558 AATGTAGTCTTATGCAATATCTTTGAGTCTTGTGCAATGTTGCAATGTTAGTACCA 2617
 QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATTTGGTGGAGTAAAGTGTACCA 120
 Db 2618 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATTTGGTGGAGTAAAGTGTACCA 2677
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTCATGATGTTGACCACTAAAT 179
 Db 2678 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTCATGATGTTGACCACTAAAT 2736
 RESULT 73
 AAD14296
 ID AAD14296 standard; DNA; 6250 BP.
 XX
 XX AAD14296;
 XX
 XX 06-NOV-2001 (first entry)
 XX
 XX MESVR/EGFP/ECFP/RSVPro(ori) vector.
 XX
 XX Transcriptional regulatory element; translational regulatory element;
 KW gene expression; diagnostic application; therapeutic application; MESVR;
 KW retrovirus vector; enhanced green fluorescent protein; EGFP; IRES;
 KW internal ribosome entry sequence; ori; origin of replication; SV40; ECFP;
 KW enhanced cyan fluorescent protein; ds.
 XX
 XX Murine embryonic stem cell virus.
 OS Rous sarcoma virus.

OS Rhesus macaque polyoma virus.
 OS Synthetic.
 OS Chimeric.
 XX
 XX WO200155371-A1.
 XX
 XX 02-AUG-2001.
 XX
 XX 26-JAN-2001; 2001WO-US002733.
 XX
 XX 28-JAN-2000; 2000US-0178816P.
 PR 02-MAR-2000; 2000US-0186496P.
 PR 30-MAY-2000; 2000US-0207804P.
 PR 07-SEP-2000; 2000US-0230852P.
 PR 07-SEP-2000; 2000US-0230956P.
 PR 12-JAN-2001; 2001US-0261312P.
 XX
 XX (Scri) SCRIPPS RES INST.
 XX
 XX Mauro VP, Edelman GM, Chappell GM, Jones FS, Owens G, Meech R;
 XX WPI; 2001-483242/52.
 XX
 XX Identifying oligonucleotides with transcriptional/translational
 PT regulatory activity in eukaryotic cells by integrating an oligonucleotide
 PT into cell genome and detecting a change in expression of expressible
 PT polynucleotides.
 XX
 XX Claim 103; Page 156-160; 172pp; English.
 XX
 XX The present invention relates to a method for the identification of an
 CC oligonucleotide with transcriptional/translational regulatory activity in
 CC a eukaryotic cell. The method involves integrating an oligonucleotide
 CC into the genome of a eukaryotic cell so that it is linked to an
 CC expressible polynucleotide or contacting the eukaryotic cell with library
 CC of vectors, obtained by cloning a library of oligonucleotide into
 CC multiple copies of expression vectors comprising polynucleotide, and
 CC detecting changes in expression of the polynucleotide. The method is
 CC useful for identifying an oligonucleotide having transcriptional or
 CC translational activity in a eukaryotic cell. It is also useful for
 CC identifying synthetic transcriptional or translational regulatory
 CC elements. The transcriptional or translational regulatory elements are
 CC useful in a variety of gene expression configurations for regulating
 CC control of expression, and in expression vectors for controlling gene
 CC expressions in diagnostic and therapeutic applications. The present
 CC sequence is MESVR/EGFP/ECFP/RSVPro(ori) vector based on Murine embryonic
 CC stem cell virus (MESV) retrovirus. The vector comprises reporter genes
 CC encoding enhanced green fluorescent protein (EGFP) and enhanced cyan
 CC fluorescent protein (ECFP). The upstream long terminal repeat (LTR)
 CC region of the retrovirus was modified to contain Rous sarcoma virus (RSV)
 CC enhancer elements. The downstream LTR region was modified to contain a
 CC multiple cloning site for the insertion of exogenous sequences that
 CC regulate transcriptional activity and the endogenous viral core promoter
 CC was replaced with a strong basal promoter. The vector also contains a
 CC simian virus 40 (SV40) origin of replication (ori) and is useful for
 CC identifying synthetic internal ribosome entry sequence (IRES) elements
 XX
 XX Sequence 6250 BP; 1474 A; 1764 C; 1611 G; 1401 T; 0 U; 0 Other;
 SQ
 Query Match 66.0%; Score 174.2; DB 4; Length 6250;
 Best Local Similarity 98.3%; Pred. No. 2.6e-50;
 Matches 176; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 AATGTAGTCTTATGCAATATCTTTGAGTCTTGTGCAATGTTGCAATGTTAGTACCA 60
 Db 3165 AATGTAGTCTTATGCAATATCTTTGAGTCTTGTGCAATGTTGCAATGTTAGTACCA 3224
 QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATTTGGTGGAGTAAAGTGTACCA 120
 Db 3225 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATTTGGTGGAGTAAAGTGTACCA 3284
 QY 121 TCGTGCCTTATTAGGAGGCAACAGACCGGCTGTCATGATGTTGACCACTAAAT 179

Search completed: March 11, 2004, 08:23:03
Job time : 231.305 secs

ALIGNMENTS

```

RESULT 1
US-09-470-881-1
; Sequence 1, Application US/09470881
; Patent No. 6685938
; GENERAL INFORMATION:
; APPLICANT: CHERESH, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
; TITLE OF INVENTION: ANGIOGENESIS AND VASCULAR PERMEABILITY USING SRC OR
; TITLE OF INVENTION: YES TYROSINE KINASES
; FILE REFERENCE: TSRI 651.2
; CURRENT APPLICATION NUMBER: US/09/470,881
; CURRENT FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US99/11780
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,220
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11627
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RCASBP (A) based
; OTHER INFORMATION: on avian sarcoma virus
; NAME/KEY: misc feature
; LOCATION: (7643)..(11258)
; OTHER INFORMATION: pBR322 sequences
; NAME/KEY: LTR
; LOCATION: (7166)..(7494)
; OTHER INFORMATION: upstream
; NAME/KEY: LTR
; LOCATION: (1)..(101)
; OTHER INFORMATION: upstream (numbering begins at the upstream R)
; NAME/KEY: misc feature
; LOCATION: (11394)..(11623)
; OTHER INFORMATION: U3
; NAME/KEY: misc feature
; LOCATION: (22)..(101)
; OTHER INFORMATION: U5
; NAME/KEY: misc feature
; LOCATION: (102)..(119)
; NAME/KEY: LTR
; LOCATION: (7166)..(7494)
; OTHER INFORMATION: downstream
; NAME/KEY: misc feature
; LOCATION: (7166)..(7393)
; OTHER INFORMATION: U3
; NAME/KEY: misc feature
; LOCATION: (7394)..(7414)
; OTHER INFORMATION: R
; NAME/KEY: misc feature
; LOCATION: (7415)..(7494)
; OTHER INFORMATION: U5
; NAME/KEY: misc feature
; LOCATION: (7154)..(7165)
; OTHER INFORMATION: PPT
; NAME/KEY: misc feature
; LOCATION: (388)..(391)
; OTHER INFORMATION: splice donor (AGGT)
; NAME/KEY: misc feature
; LOCATION: (5074)..(5077)
; OTHER INFORMATION: env splice acceptor (AGGC)
; NAME/KEY: misc feature

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; LOCATION: (6982)..(6985)
; OTHER INFORMATION: Clai splice acceptor (AGGA)
; NAME/KEY: gene
; LOCATION: (372)..(902)
; OTHER INFORMATION: gag p19
; NAME/KEY: gene
; LOCATION: (909)..(1094)
; OTHER INFORMATION: gag p10
; NAME/KEY: gene
; LOCATION: (1095)..(1814)
; OTHER INFORMATION: gag p27
; NAME/KEY: gene
; LOCATION: (1843)..(2108)
; OTHER INFORMATION: gag p12
; NAME/KEY: gene
; LOCATION: (2109)..(2480)
; OTHER INFORMATION: gag p15
; NAME/KEY: misc signal
; LOCATION: (2481)..(2483)
; OTHER INFORMATION: gag stop
; NAME/KEY: gene
; LOCATION: (2501)..(4216)
; OTHER INFORMATION: pol RT
; NAME/KEY: Gene
; LOCATION: (4217)..(5185)
; OTHER INFORMATION: pol IN
; NAME/KEY: misc signal
; LOCATION: (5186)..(5188)
; OTHER INFORMATION: pol stop
; NAME/KEY: Gene
; LOCATION: (5244)..(6263)
; OTHER INFORMATION: env gp85
; NAME/KEY: Gene
; LOCATION: (6264)..(6878)
; OTHER INFORMATION: env gp37
; NAME/KEY: misc signal
; LOCATION: (6879)..(6881)
; OTHER INFORMATION: env stop
; NAME/KEY: misc feature
; LOCATION: (7027)
; OTHER INFORMATION: Clai site/ the Clai site in gag is methylated in
; OTHER INFORMATION: Dam+ strains and does not cut
US-09-470-881-1

Query Match 99.0%; Score 261.4; DB 4; Length 11627;
Best Local Similarity 99.6%; Pred. No. 4.6e-82;
Matches 262; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGTAACCATGAGTTAGCAACA 60
Db 7166 AATGAGTCTTATGCAATACCTCTTGTAGTCTTGCAACATGTAACCATGAGTTAGCAACA 7225

QY 61 TGCCTTACAGGAGACAAAAGCACCGTCATGCCGATTGGTGAAGTAAGTGTACGA 120
Db 7226 TGCCTTACAGGAGACAAAAGCACCGTCATGCCGATTGGTGAAGTAAGTGTACGA 7285

QY 121 TCGTGCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 180
Db 7286 TCGTGCCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 7345

QY 181 CCGCATTCGACAGATATTGTATTAACTGCTAGCTAGCTGATACATATAAGCCATTGGACC 240
Db 7346 CCGCATTCGACAGATATTGTATTAACTGCTAGCTAGCTGATACATATAAGCCATTGGACC 7405

QY 241 ATTCCACCACATTGGTGTGCACCT 263
Db 7406 ATTCCACCACATTGGTGTGCACCT 7428

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```

RESULT 2
US-08-564-313-1
; Sequence 1, Application US/08564313
; Patent No. 5910488

```

GENERAL INFORMATION:
 APPLICANT: Nabel, Elizabeth
 APPLICANT: Nabel, Gary
 APPLICANT: Lew, Denise
 APPLICANT: Marquet, Magda
 TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson and Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: USA
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.1
 CURRENT APPLICATION DATA:
 FILING DATE: 01-DEC-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/074,344
 FILING DATE: 07-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Israel, Ned
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: VICAL.033CP1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-235-8550
 TELEFAX: 619-235-0176
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4965 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 IMMEDIATE SOURCE:
 CLONE: HLA-B7 and Beta-2
 US-08-564-313-1

Query Match 97.6%; Score 257.6; DB 2; Length 4965;
 Best Local Similarity 98.5%; Pred. No. 6.9e-81;
 Matches 260; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AATGTAGCTTTATGCAATACCTCTTTGTTAGTCTTTCGCAACATGTAAGTACGATGAGTACCA 60
 Db 260 AATGTAGCTTTATGCAATACCTCTTTGTTAGTCTTTCGCAACATGTAAGTACGATGAGTACCA 319
 QY 61 TGCCTTACAGGAG 120
 Db 320 TGCCTTACAGGAG 379
 QY 121 TCGTGCCTTTATGAG 180
 Db 380 TCGTGCCTTTATGAG 439
 QY 181 CCGCATTTGACAGAGATATTGTATTAAAGTCCCTAGCTGATACAAATAAAGCCATTGACC 240
 Db 440 CCGCATTTGACAGAGATATTGTATTAAAGTCCCTAGCTGATACAAATAAAGCCATTGACC 499
 QY 241 ATTCACACATTTGGTGGACCTC 264
 Db 500 ATTCACACATTTGGTGGACCTC 523

RESULT 3
 PCT-US94-06069-1
 Sequence 1, Application PC/TUS9406069
 GENERAL INFORMATION:
 APPLICANT: Vical Incorporated
 APPLICANT: Regents of the University of Michigan
 APPLICANT: Nabel, Elizabeth
 APPLICANT: Nabel, Gary
 APPLICANT: Lew, Denise
 APPLICANT: Marquet, Magda
 TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson and Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: USA
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/06069
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/074,344
 FILING DATE: 07-JUN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Israel, Ned
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: VICAL.033VPC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-235-8550
 TELEFAX: 619-235-0176
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4965 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 STRAIN: HLA-B7 and Beta-2
 PCT-US94-06069-1

Query Match 97.6%; Score 257.6; DB 5; Length 4965;
 Best Local Similarity 98.5%; Pred. No. 6.9e-81;
 Matches 260; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 AATGTAGCTTTATGCAATACCTCTTTGTTAGTCTTTCGCAACATGTAAGTACGATGAGTACCA 60
 Db 260 AATGTAGCTTTATGCAATACCTCTTTGTTAGTCTTTCGCAACATGTAAGTACGATGAGTACCA 319
 QY 61 TGCCTTACAGGAG 120
 Db 320 TGCCTTACAGGAG 379
 QY 121 TCGTGCCTTTATGAG 180
 Db 380 TCGTGCCTTTATGAG 439
 QY 181 CCGCATTTGACAGAGATATTGTATTAAAGTCCCTAGCTGATACAAATAAAGCCATTGACC 240
 Db 440 CCGCATTTGACAGAGATATTGTATTAAAGTCCCTAGCTGATACAAATAAAGCCATTGACC 499

QY 241 ATTACACACATTGGTGTGCACCTC 264
 DB 500 ATTACACACATTGGTGTGCACCTC 523

RESULT 4
 US-08-564-313-2/c
 ; Sequence 2, Application US/08564313
 ; Patent No. 5910488
 ; GENERAL INFORMATION:
 ; APPLICANT: Nabel, Elizabeth
 ; APPLICANT: Nabel, Gary
 ; APPLICANT: Lew, Denise
 ; APPLICANT: Marquet, Magda
 ; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: Fast-SEQ Version 1.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/564,313
 ; FILING DATE: 01-DEC-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/074,344
 ; FILING DATE: 07-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israel, Ned
 ; REGISTRATION NUMBER: 29,655
 ; REFERENCE/DOCKET NUMBER: VICAL.033CPI
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8550
 ; TELEFAX: 619-235-0176
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4059 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; IMMEDIATE SOURCE:
 ; CLONE: HLA-B7
 ; US-08-564-313-2

Query Match 94.0%; Score 248.2; DB 2; Length 4059;
 Best Local Similarity 98.5%; Pred. No. 1.3e-77;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGGTAAGTGTAGCAACA 60
 DB 3156 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGGTAAGTGTAGCAACA 3097
 QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATGGTGAAGTGTAGCA 120
 DB 3096 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATGGTGAAGTGTAGCA 3037
 QY 121 TCGTGCCTTATTAGGAAGGCAACAGACCGGTCTGACATGATTGGACCAACCACTAAATT 180
 DB 3036 TCGTGCCTTATTAGGAAGGCAACAGACCGGTCTGACATGATTGGACCAACCACTAAATT 2977

QY 181 CCGCATTGCAGAGAT-AATGTATTTAAGTCCCTAGCTCGATCAATAAAGCCCAATTGAC 239
 DB 2976 CCGCATTGCAGAGAT-AATGTATTTAAGTCCCTAGCTCGATCAATAAAGCCCAATTGAC 2917
 QY 240 CATTACACACATTGGTGTGCACCTC 264
 DB 2916 CATTACACACATTGGTGTGCACCTC 2892
 RESULT 5
 PCT-US94-06069-2/c
 ; Sequence 2, Application PC/TUS9406069
 ; GENERAL INFORMATION:
 ; APPLICANT: Vical Incorporated
 ; APPLICANT: Regents of the University of Michigan
 ; APPLICANT: Nabel, Elizabeth
 ; APPLICANT: Nabel, Gary
 ; APPLICANT: Lew, Denise
 ; APPLICANT: Marquet, Magda
 ; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson and Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: Fast-SEQ Version 1.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/06069
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/074,344
 ; FILING DATE: 07-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israel, Ned
 ; REGISTRATION NUMBER: 29,655
 ; REFERENCE/DOCKET NUMBER: VICAL.033VPC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-235-8550
 ; TELEFAX: 619-235-0176
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4059 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; STRAIN: HLA-B7
 ; PCT-US94-06069-2
 Query Match 94.0%; Score 248.2; DB 5; Length 4059;
 Best Local Similarity 98.5%; Pred. No. 1.3e-77;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGGTAAGTGTAGCAACA 60
 DB 3156 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAACATGGTAAGTGTAGCAACA 3097
 QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATGGTGAAGTGTAGCA 120
 DB 3096 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATGGTGAAGTGTAGCA 3037

; ORGANISM: Homo sapiens
US-09-481-355-18

Query Match 94.0%; Score 248.2; DB 4; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1.7e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACTCTTGTTAGTCTTGCAACATGGTAACGATGAGTTAGCAACA 60
|||
Db 1558 AATGTAGTCTTATGCAATACTCTTGTTAGTCTTGCAACATGGTAACGATGAGTTAGCAACA 1617

Qy 61 TGCCCTTACAAAGGACAGAAAAGCACCCGTGCATGCCGATTGGTGGAAAGTANGGTGGTACGA 120
|||
Db 1618 TGCCCTTACAAAGGACAGAAAAGCACCCGTGCATGCCGATTGGTGGAAAGTANGGTGGTACGA 1677

Oy 121 TCGTGCCTTTATTAGGAAGGCAACAGACGGGTCTGCATGGATTGGACGACCATAAATT 180
|||||
D6 1678 TCSTGCCCTTATTAGGAAGGCAACAGACAGGTCGTACATCGATTGGACGACCATTGAATT 1737
|||||

Qy 181 CCGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGTCCGATACAAATAACGCCATTTCAC 239
|||
Db 1738 CCGCATTCGACAGACATAATTGCTATTATTAAGTGCCTAGTCCGATACAAATAACGCCATTTCAC 1787

QY 240 CATTACCCACATTGGTGTGCACCTC 264
|||||
DB 1700 GATTTGTCCTGCTTTTCCTGCTGCTG 1822

RESULT 11

Sequence 18, Application US/09481282
Patent No. 6541221
GENERAL INFORMATION:

```

; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

```

; TITLE OF INVENTION: ENDOGENOUS GENES
 ; FILE REFERENCE: 0221-0003US
 ; CURRENT APPLICATION NUMBER: US/09/481,282
 ; CURRENT FILING DATE: 2000-01-11

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; ERROR APPLICATION NUMBER: 09/159,643
;
; PRIOR FILING DATE: 1998-09-24
;
; PRIOR APPLICATION NUMBER: 08/941,223
;
; PRIOR FILING DATE: 1997-09-26
;

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; PRIOR APPLICATION NUMBER: 09/263,814
 ;
 ; PRIOR FILING DATE: 1999-03-08
 ;
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ;
 ; PRIOR FILING DATE: 1999-02-19
 ;

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; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836

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; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-481-282-18

Query Match 94.0%; Score 248.2; DB 4; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1.7e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCCTTATGCCAAATACCTCTTTGTAGTCCTTGCAACATGGTAACGATGAGTTAGCAACA 60

Db 1558 AATGTAGTCCTTATGCCAAATACCTCTTTGTAGTCCTTGCAACATGGTAACGATGAGTTAGCAACA 1617

Qy 61 TGCCTTACAAGGAGAGAAAAAGCACCGTCATGCCGATTGGTGGAAAGTAAGGTGGTACGA 120

Db 1618 TGCCTTACAAGGAGAGAAAAAGCACCGTCATGCCGATTGGTGGAAAGTAAGGTGGTACGA 1677

Qy 121 TCGTGCCTTATTAGGAAGSCACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 180
|||
Db 1678 TCGTGCCTTATTAGGAAGSCACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 1737

;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
;/ TITLE OF INVENTION: ENDOGENOUS GENES
;/ FILE REFERENCE: 0221-0003H
;/ CURRENT APPLICATION NUMBER: US/09/484,996
;/ PRIOR FILING DATE: 2000-01-18
;/ PRIOR APPLICATION NUMBER: 09/276,820
;/ PRIOR FILING DATE: 1999-03-26
;/ PRIOR APPLICATION NUMBER: 09/263,814
;/ PRIOR FILING DATE: 1998-03-08
;/ PRIOR APPLICATION NUMBER: 09/253,022
;/ PRIOR FILING DATE: 1999-02-19
;/ PRIOR APPLICATION NUMBER: 09/159,643
;/ PRIOR FILING DATE: 1998-09-24
;/ PRIOR APPLICATION NUMBER: 08/941,223
;/ PRIOR FILING DATE: 1997-09-26
;/ NUMBER OF SEQ ID NOS: 33
;/ SOFTWARE: PatentIn Ver. 2.1
;/ SEQ ID NO 18
;/ LENGTH: 6836
;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ US-09-484-996-18

Query Match 94.0%; Score 248.2; DB 4; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1.7e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
DB 1558 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAGAAAAGCACCCGTCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
DB 1618 TGCCTTACAGGAGAGAGAAAAGCACCCGTCATGCCGATTTGGTGAAGTAAGTGGTACGA 1677
QY 121 TCGTGCCTTATTAGAAGGCAACAGACGGGCTCTGACATGATTTGGACGAGAACCACTAAATT 180
DB 1678 TCGTGCCTTATTAGAAGGCAACAGACGGGCTCTGACATGATTTGGACGAGAACCACTAAATT 1737
QY 181 CGCATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAAAGCCCACTTTGAC 239
DB 1738 CGCATTCGAGAGATTAATTGATTATTTAGTGCCTAGCTCGATACATAAAGCCCACTTTGAC 1797
QY 240 CATTCCACCACATTTGGTGCACCTC 264
DB 1798 CATTCCACCACATTTGGTGCACCTC 1822

RESULT 14
US-09-479-123-18
;/ Sequence 18, Application US/09479123
;/ Patent No. 6670185
;/ GENERAL INFORMATION:
;/ APPLICANT: HARRINGTON, JOHN J.
;/ APPLICANT: SHERP, BRUCE
;/ APPLICANT: KUNDLETT, STEPHEN
;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
;/ TITLE OF INVENTION: ENDOGENOUS GENES
;/ FILE REFERENCE: 0221-0003B
;/ CURRENT APPLICATION NUMBER: US/09/479,123
;/ PRIOR FILING DATE: 2000-01-07
;/ PRIOR APPLICATION NUMBER: 09/263,814
;/ PRIOR FILING DATE: 1999-03-08
;/ PRIOR APPLICATION NUMBER: 09/253,022
;/ PRIOR FILING DATE: 1999-02-19
;/ PRIOR APPLICATION NUMBER: 09/159,643
;/ PRIOR FILING DATE: 1998-09-24
;/ PRIOR APPLICATION NUMBER: 08/941,223
;/ PRIOR FILING DATE: 1997-09-26
;/ NUMBER OF SEQ ID NOS: 33
;/ SOFTWARE: PatentIn Ver. 2.1
;/ SEQ ID NO 18
;/ LENGTH: 6836

;/ TYPE: DNA
;/ ORGANISM: Homo sapiens
;/ US-09-479-123-18
Query Match 94.0%; Score 248.2; DB 4; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1.7e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 60
DB 1558 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGGCAATGTAACGATGAGTTAGCAACA 1617
QY 61 TGCCTTACAGGAGAGAGAAAAGCACCCGTCATGCCGATTTGGTGAAGTAAGTGGTACGA 120
DB 1618 TGCCTTACAGGAGAGAGAAAAGCACCCGTCATGCCGATTTGGTGAAGTAAGTGGTACGA 1677
QY 121 TCGTGCCTTATTAGAAGGCAACAGACGGGCTCTGACATGATTTGGACGAGAACCACTAAATT 180
DB 1678 TCGTGCCTTATTAGAAGGCAACAGACGGGCTCTGACATGATTTGGACGAGAACCACTAAATT 1737
QY 181 CGCATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAAAGCCCACTTTGAC 239
DB 1738 CGCATTCGAGAGATTAATTGATTATTTAGTGCCTAGCTCGATACATAAAGCCCACTTTGAC 1797
QY 240 CATTCCACCACATTTGGTGCACCTC 264
DB 1798 CATTCCACCACATTTGGTGCACCTC 1822

RESULT 15
US-08-462-859A-6
;/ Sequence 6, Application US/08462859A
;/ Patent No. 5652092
;/ GENERAL INFORMATION:
;/ APPLICANT: Jacobsen, J. S.
;/ APPLICANT: Vittek, M. P.
;/ TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
;/ TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
;/ TITLE OF INVENTION: of B-Amyloid Peptide
;/ NUMBER OF SEQUENCES: 19
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSER: American Cyanamid Company
;/ STREET: One Cyanamid Plaza
;/ CITY: Wayne
;/ STATE: New Jersey
;/ COUNTRY: United States
;/ ZIP: 07470-8426
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/462,859A
;/ FILING DATE: 05-JUN-1995
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Barnhard, Elizabeth M.
;/ REGISTRATION NUMBER: 31,088
;/ REFERENCE/DOCKET NUMBER: 31,844-04
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (201)831-3246
;/ TELEFAX: (201)831-3305
;/ INFORMATION FOR SEQ ID NO: 6:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 8591 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: double
;/ TOPOLOGY: circular
;/ MOLECULE TYPE: cDNA
;/ FEATURE:
;/ NAME/KEY: CDS
;/ LOCATION: 2393..3868

US-08-462-859A-6

Query Match 94.0%; Score 248.2; DB 1; Length 8591;
Best Local Similarity 98.5%; Pred.No. 1.8e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1;

Qy	1	AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGCTAAACGATGAGTATTAGCAACA	60
Db	4975	AATGTAGTCTTATGCAATACACTCTTGTAGTCTTGTGCAACATGCTAAACGATGAGTATTAGCAACA	5034
Qy	61	TGCCTTCAACAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAAGGTGGTTCACA	120
Db	5035	TGCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAAGGTGGTTCACA	5094
Qy	121	TGTGTCCTTTATTAGGAAGGCACAGACGGGTCTTGCATGTGATTGGAACGACCACTAAATTT	180
Db	5095	TGTGTCCTTTATTAGGAAGGCACAGACAGGCTCTGCATGTGATTGGAACGACCACTGAATTT	5154
Qy	181	CGCATTTGCAGAGAT -ATTGTATTAAAGTGCTAGCTGCATACAAATAAGCCATTTCAC	239
Db	5155	CGCATTTGCAGAGATTAATTGATTAAAGTGCTAGCTGCATACAAATAAGCCATTTCAC	5214
Qy	240	CAATTACCAACATTTGGTGTGCACCTC	264
Db	5215	CAATTACCAACATTTGGTGTGCACCTC	5239

RESULT 16

US-08-462-859A-8
: Sequence 8, Application US/08462859A

PATENT NO. 5552092
 GENERAL INFORMATION:
 APPLICANT: Jacobsen, J. S.
 APPLICANT: Vitek, M. P.
 TITLE OF INVENTION: No. 552092el Amyloid Precursor and Method of
 TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
 TITLE OF INVENTION: of B-Amyloid Peptide
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne

LOCATION:
US-08-462-859A-8

Query Match	94.0%;	Score 248.2;	DB 1;	Length 8591;
Best Local Similarity	98.5%;	Pred. No. 1.8e-77;		

Query Match	94.0%;	Score	248.2;	DB	1;	Length	8591;
Best Local Similarity	98.5%;	Prod.	No. 1.8e-77;				
Matches	261;	Conservative	0;	Mismatches	3;	Indels	1;
QY	1	AATGTAGTCTTATGCAATACTCTTTGTAGTCTTGCACATGGTAAACGATGAGTTAGCAACA	60				
Db	4975	AATGTAGTCTTATGCAATACACTTTGTAGTCTTGCACATGGTAAACGATGAGTTAGCAACA	5034				
QY	61	TGCCTTACAGAGAGAAAAGCACCGTGCGATCCGCAATGGTGGAGTFRAGTGTCAGA	120				
Db	5035	TGCCTTACAGAGAGAAAAGCACCGTGCGATCCGCAATGGTGGAGTFRAGTGTCAGA	5094				
QY	121	TGCTGCCTTATTAGGAAGCAACAGACGGGTCTGCATCGAATTGACGAACCACTAAATTT	180				
Db	5095	TGCTGCCTTATTAGGAAGCAACAGACAGGCTCTGCATCGAATTGACGAACCACTGAATTT	5154				
QY	181	CGGCATTCGAGAGAT-ATTGTATTTAAGTCGCTAGCTCGATACATAAAGCGCATTTGCAC	239				
Db	5155	CGGCATTCGAGAGAT-ATTGTATTTAAGTCGCTAGCTCGATACATAAAGCGCATTTGCAC	5214				
QY	240	CATTACACCAATGGTGTGCACCTC	264				
Db	5215	CATTACACCAATGGTGTGCACCTC	5239				

RESULT 17

US-08-123-659A-6
; Sequence 6, Application US/08123659A

Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.

Query Match	94.0%;	Score 248.2;	DB 1;	Length 8591;
Best Local Similarity	98.5%;	Pred. No. 1.8e-77;		

Matches	261;	Conservative	0;	Mismatches	3;	Indels	1;	Gaps	1;
Qy	1	AATGTAGCTTTATGCAATACTCTTGTAGTCTTGGCAACATGGTAAACGATGAGTTAGCAACA	60						
Ddb	4975	AATGTAGCTTTATGCAATACACTTGTAGTCTTGGCAACATGGTAAACGATGAGTTAGCAACA	5034						
Qy	61	TGCTTACAGAGGAGAAAGACACCGTGCATGCCGATTTGGTGGAGGTAAAGTGTGTGACGA	120						
Ddb	5035	TGCTTACAGAGGAGAAAGACACCGTGCATGCCGATTTGGTGGAGGTAAAGTGTGTGACGA	5094						
Qy	121	TGTCGCTCTTATGGAAGGCAACAGACGGCTCGACATCGATTGGACAAACCACTAAATT	180						
Ddb	5095	TGTCGCTCTTATGGAAGGCAACAGACAGGCTCGACATCGATTGGACAAACCACTGAATT	5154						
Qy	181	CGCATGTCAGACAGAT-ATTGTATTAAAGTGCTAGCTCGATACATAAAGCCGCAATTTCAC	239						
Ddb	5155	CGCATGTCAGAGATTAATTGTATTAAAGTGCTAGCTCGATACATAAAGCCGCAATTTCAC	5214						
Qy	240	CATTCAACCAATTTGGTGTGCACCTC	264						
Ddb	5215	CATTCAACCAATTTGGTGTGCACCTC	5239						

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RESULT 18
US-08-123-659A-8
; Sequence 8, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, N. P. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518) 475-0611
; TELEFAX: (518) 475-0619
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3853
US-08-123-659A-8

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QY	1	AAATGTAAGTCTTATGCGAATGACTCTTTGTAAGTCTTTCACACATGGTAAAGTATGAGTTAGCAACA	60
Db	4975	AAATGTAAGTCTTATGCGAATGACTCTTTGTAAGTCTTTCACACATGGTAAAGTATGAGTTAGCAACA	5034
QY	61	TGCCTTTACAGGAGAGAAAAAGCACCGGTGCATGCCGATTGGTGGAAAGTAAAGGTGGTACGA	120
Db	5035	TGCCTTTACAGGAGAGAAAAAGCACCGGTGCATGCCGATTGGTGGAAAGTAAAGGTGGTACGA	5094
QY	121	TGCTGCCCTTATTAGGAGGCAACACAGACGGGTCTGCATGTGGATTTGGACGACCACTAAATT	180
Db	5095	TGCTGCCCTTATTAGGAGGCAACACAGACGGGTCTGCATGTGGATTTGGACGACCACTAAATT	5154
QY	181	CGCGATTGCAGAGAT-ATTGTATTATTAAAGTGCCCTAGCTCGATACATAAATAAAGCCCAATTGAC	239
Db	5155	CGCGATTGCAGAGATATTGTATTATTAAAGTGCCCTAGCTCGATACATAAAGCCCAATTGAC	5214
QY	240	CATTCCACCATTGGTGTGCCAAGTC	264
Db	5215	CATTCCACCATTGGTGTGCCAAGTC	5239

RESULT 19
 US-08-464-247A-6
 ; Sequence 6, Application US/08464247A
 ; Patent No. 5693478
 ; GENERAL INFORMATION:
 ; APPLICANT: Vitek, M. P.
 ; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
 ; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
 ; TITLE OF INVENTION: of B-Amyloid Peptide
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: American Cyanamid Company
 ; STREET: One Campus Drive
 ; CITY: Parsippany
 ; STATE: New Jersey
 ; COUNTRY: United States
 ; ZIP: 07054
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/464,247A
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Barnhard, Elizabeth M.
 ; REGISTRATION NUMBER: 31,088
 ; REFERENCE/DOCKET NUMBER: 31,844-03
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-683-2158
 ; TELEFAX: 201-683-4117
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8591 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 2393..3869
 ; US-08-464-247A-6

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Query Match      94.0%; Score 248.2; DB 1; Length 8591;
Best Local Similarity 98.5%; Pred. No. 1.4e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

CY      1 AATGTACTCTTATGCAATACTCTTGTACTCTTGCAACGTGTAACTAGTGTAGCAACA 60

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Db 5035 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 5094
Qy 121 TCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 180
Db 5095 TCGTGCCTTATTAGAGAGGCAACAGACAGGTCTGACATGGATTGGACGACCACTAAATT 5154
Qy 181 CCGCATTGACAGAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 239
Db 5155 CCGCATTGACAGAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 5214
Qy 240 CATTACACCACTTGGTGTGCACCTC 264
Db 5215 CATTACACCACTTGGTGTGCACCTC 5239
RESULT 22
US-08-464-248A-8
; Sequence 8, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,248A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3853
US-08-464-248A-8
Query Match 94.0%; Score 248.2; DB 1; Length 8591;
Best Local Similarity 98.5%; Pred. No. 1.8e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGCTTATTAGCAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 60
Db 4975 AATGTAGCTTATTAGCAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 5034
Qy 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 120
Db 5035 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 5094

Qy 121 TCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 180
Db 5095 TCGTGCCTTATTAGAGAGGCAACAGACAGGTCTGACATGGATTGGACGACCACTAAATT 5154
Qy 181 CCGCATTGACAGAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 239
Db 5155 CCGCATTGACAGAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 5214
Qy 240 CATTACACCACTTGGTGTGCACCTC 264
Db 5215 CATTACACCACTTGGTGTGCACCTC 5239
RESULT 23
US-09-479-122-22
; Sequence 22, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0803C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-22
Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGCTTATTAGCAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 60
Db 1411 AATGTAGCTTATTAGCAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 1470
Qy 61 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAAGCACCGTGCATGCCGATGCTGGAGTAAGGTGGTACGA 1530
Qy 121 TCGTGCCTTATTAGAGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 180
Db 1531 TCGTGCCTTATTAGAGAGGCAACAGACAGGTCTGACATGGATTGGACGACCACTAAATT 1590
Qy 181 CCGCATTGACAGAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 239
Db 1591 CCGCATTGACAGAGAT-ATTGTATTATTAGTCTGCTAGCTCGATACATAAAGCCATTGGAC 1650
Qy 240 CATTACACCACTTGGTGTGCACCTC 264

Db 1651 CATTCAACACATGGTGTGCACCTC 1675

RESULT 24

US-09-479-122-23
; Sequence 23, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-23

Query Match 94.0%; Score 248.2; DB 4; Length 9737;

Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGCTGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGCTGTAACGATGAGTTAGCAACA 1470
Qy 61 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCGGATTTGGTGAAGTAAGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCGGATTTGGTGAAGTAAGTGGTACGA 1530
Qy 121 TCGTGCTTATTAGGAGGCAACGAGCGGCTGACATGATGATGGAACCACTAAATT 180
Db 1531 TCGTGCTTATTAGGAGGCAACGAGCGGCTGACATGATGATGGAACCACTAAATT 1590
Qy 181 CCGCATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAAATACGCAATTGAC 239
Db 1591 CCGCATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAAATACGCAATTGAC 1650
Qy 240 CATTCAACACATGGTGTGCACCTC 264
Db 1651 CATTCAACACATGGTGTGCACCTC 1675

RESULT 25

US-09-479-122-28
; Sequence 28, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-28

Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGCTGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTTGCAACATGCTGTAACGATGAGTTAGCAACA 1470
Qy 61 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCGGATTTGGTGAAGTAAGTGGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCGGATTTGGTGAAGTAAGTGGTACGA 1530
Qy 121 TCGTGCTTATTAGGAGGCAACGAGCGGCTGACATGATGATGGAACCACTAAATT 180
Db 1531 TCGTGCTTATTAGGAGGCAACGAGCGGCTGACATGATGATGGAACCACTAAATT 1590
Qy 181 CCGCATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAAATACGCAATTGAC 239
Db 1591 CCGCATTCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACATAAATACGCAATTGAC 1650
Qy 240 CATTCAACACATGGTGTGCACCTC 264
Db 1651 CATTCAACACATGGTGTGCACCTC 1675

RESULT 26

US-09-484-997-22
; Sequence 22, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 9737
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (8347)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 ; NAME/KEY: modified_base
 ; LOCATION: (8499)
 ; OTHER INFORMATION: a, c, t, g, other or unknown
 US-09-484-997-22

 Query Match 94.0%; Score 248.2; DB 4; Length 9737;
 Best Local Similarity 98.5%; Pred.No.1.9e-77;
 Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

 QY 1 AATGTAGTCCTTATGCACATCTCTTGAGCTCTTGCACACATGCTAACGATGAGTTAGCAACA 60
 Db 1411 AATGTAGTCCTTATGCACATCTCTTGAGCTCTTGCACACATGCTAACGATGAGTTAGCAACA 1470

 QY 61 TGCCTTACAGGAGAGAAAAAGCACCGTGCTGCGATGCGGATTCGGTGAAGTAAGTGGTGTACGA 120
 Db 1471 TGCCTTACAGGAGAGAAAAAGCACCGTGCTGCGATGCGGATTCGGTGAAGTAAGTGGTGTACGA 1530

 QY 121 TGTGTCCTTATTAGGAGGCAACAGACGGGCTCTGCATGCTGACATGCTGACATGCTGACATGCTGACATGCTGACATGCTGACAT 180
 Db 1531 TGTGTCCTTATTAGGAGGCAACAGACGGGCTCTGCATGCTGACATGCTGACATGCTGACATGCTGACATGCTGACAT 1590

 QY 181 CGCGATTGCAGAGAT-ATTGTATTTAAGTGCTCTAGCTCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 239
 Db 1591 CGCGATTGCAGAGATTAATTGTATTTAAGTGCTCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 1650

 QY 240 CATTCCACCACATGGGTGTCACCTC 264
 Db 1651 CATTCCACCACATGGGTGTCACCTC 1675

 RESULT 27
 US-09-484-997-23
 ; Sequence 23, Application US/09484997
 ; Patent No. 6524818
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHEFF, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; TITLE OF INVENTION: ENDOGENOUS GENES
 ; FILE REFERENCE: 0221-0003J
 ; CURRENT APPLICATION NUMBER: US/09/484,997
 ; CURRENT FILING DATE: 2000-01-18
 ; PRIOR APPLICATION NUMBER: 09/276,820
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 09/159,643
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 9737

Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTCGTGGAAGTAAGTGTGACGA 120
Db 1471 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTCGTGGAAGTAAGTGTGACGA 1530

Qy 121 TCGTGCCCTTATTAGGAGCAACAGACAGGCTCTGACATGATTCGACATTAACCACTAAATT 180
Db 1531 TCGTGCCCTTATTAGGAGCAACAGACAGGCTCTGACATGATTCGACATTAACCACTAAATT 1590

Qy 181 CCGCATTGCGAGAGAT-ATTGTATTATTAGTGCCTGATCGATACATAATAAAGCCATTTCAC 239
Db 1591 CCGCATTGCGAGAGAT-ATTGTATTATTAGTGCCTGATCGATACATAATAAAGCCATTTCAC 239

Qy 240 CATTCACCACATTGGTGTGCACCTC 264
Db 1651 CATTCACCACATTGGTGTGCACCTC 1675

RESULT 29
US-09-481-355-22
; Sequence 22, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-22

Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTCGTGGAAGTAAGTGTGACGA 120
Db 1471 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTCGTGGAAGTAAGTGTGACGA 1530

Qy 121 TCGTGCCCTTATTAGGAGCAACAGACAGGCTCTGACATGATTCGACATTAACCACTAAATT 180
Db 1531 TCGTGCCCTTATTAGGAGCAACAGACAGGCTCTGACATGATTCGACATTAACCACTAAATT 1590

Qy 181 CCGCATTGCGAGAGAT-ATTGTATTATTAGTGCCTGATCGATACATAATAAAGCCATTTCAC 239
Db 1591 CCGCATTGCGAGAGAT-ATTGTATTATTAGTGCCTGATCGATACATAATAAAGCCATTTCAC 239

Qy 240 CATTCACCACATTGGTGTGCACCTC 264
Db 1651 CATTCACCACATTGGTGTGCACCTC 1675

Db 1471 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTCGTGGAAGTAAGTGTGACGA 1530
Qy 121 TCGTGCCCTTATTAGGAGCAACAGACAGGCTCTGACATGATTCGACATTAACCACTAAATT 180
Db 1531 TCGTGCCCTTATTAGGAGCAACAGACAGGCTCTGACATGATTCGACATTAACCACTAAATT 1590
Qy 181 CCGCATTGCGAGAGAT-ATTGTATTATTAGTGCCTGATCGATACATAATAAAGCCATTTCAC 239
Db 1591 CCGCATTGCGAGAGAT-ATTGTATTATTAGTGCCTGATCGATACATAATAAAGCCATTTCAC 239
Qy 240 CATTCACCACATTGGTGTGCACCTC 264
Db 1651 CATTCACCACATTGGTGTGCACCTC 1675

RESULT 30
US-09-481-355-23
; Sequence 23, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-23

Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACACTCTTTAGTCTTTGCAACATGGTAACGATGAGTTAGCAACA 1470

Qy 61 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTCGTGGAAGTAAGTGTGACGA 120
Db 1471 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTCGTGGAAGTAAGTGTGACGA 1530

Qy 121 TCGTGCCCTTATTAGGAGCAACAGACAGGCTCTGACATGATTCGACATTAACCACTAAATT 180
Db 1531 TCGTGCCCTTATTAGGAGCAACAGACAGGCTCTGACATGATTCGACATTAACCACTAAATT 1590

Qy 181 CCGCATTGCGAGAGAT-ATTGTATTATTAGTGCCTGATCGATACATAATAAAGCCATTTCAC 239
Db 1591 CCGCATTGCGAGAGAT-ATTGTATTATTAGTGCCTGATCGATACATAATAAAGCCATTTCAC 239

Qy 240 CATTCACCACATTGGTGTGCACCTC 264
Db 1651 CATTCACCACATTGGTGTGCACCTC 1675


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; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-23

Query Match          94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
    |||||
DB 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTTGGTGAAGTAAAGTGTACGA 120
    |||||
DB 1471 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTTGGTGAAGTAAAGTGTACGA 1530

QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTTGACATGGATTGGACGAAACCACTAAATT 180
    |||||
DB 1531 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTTGACATGGATTGGACGAAACCACTAAATT 1590

QY 181 CGCGATTCGACAGAT-ATTGTATTATTAGTCCCTAGCTCGATACATTAACGCGCATTTCAC 239
    |||||
DB 1591 CGCGATTCGACAGATTAATTGTATTATTAGTCCCTAGCTCGATACATTAACGCGCATTTCAC 1650

QY 240 CATTCAACACATTTGGTGTGCACCTC 264
    |||||
DB 1651 CATTCAACACATTTGGTGTGCACCTC 1675

RESULT 34
US-09-481-282-28
; Sequence 28, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
```

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-28

Query Match          94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
    |||||
DB 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTTGGTGAAGTAAAGTGTACGA 120
    |||||
DB 1471 TGCCTTACAGAGAGAGAAAGCAACCGTGCATGCGGATTTGGTGAAGTAAAGTGTACGA 1530

QY 121 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTTGACATGGATTGGACGAAACCACTAAATT 180
    |||||
DB 1531 TCGTGCCCTTATTAGGAGGCAACAGACGGGTCTTGACATGGATTGGACGAAACCACTAAATT 1590

QY 181 CGCGATTCGACAGAT-ATTGTATTATTAGTCCCTAGCTCGATACATTAACGCGCATTTCAC 239
    |||||
DB 1591 CGCGATTCGACAGATTAATTGTATTATTAGTCCCTAGCTCGATACATTAACGCGCATTTCAC 1650

QY 240 CATTCAACACATTTGGTGTGCACCTC 264
    |||||
DB 1651 CATTCAACACATTTGGTGTGCACCTC 1675

RESULT 35
US-09-455-659A-22
; Sequence 22, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
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Qy 181 CCGCATTCGACAGAT-ATTGPTATTAAGTGCCTAGCTCGATACAAATAAACCCCATTTGAC 239
Db 1591 CCGCATTCGACAGATAATTGTTATTAAGTGCCTAGCTCGATACAAATAAACCCCATTTGAC 1650
Qy 240 CATTCCACCATTTGGTGTGCACCTC 264
Db 1651 CATTCCACCATTTGGTGTGCACCTC 1675

RESULT 38

US-09-484-996-22
; Sequence 22, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-22

Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTTAAGCATGATGATTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTTAAGCATGATGATTTAGCAACA 1470
Qy 61 TGCCTTACAAGAGAGAAAGAACCCGTCATGCCGATTTGGTGAAGTAAGTGTACGA 120
Db 1471 TGCCTTACAAGAGAGAAAGAACCCGTCATGCCGATTTGGTGAAGTAAGTGTACGA 1530
Qy 121 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGACATGATTTGGACGAACCACTAAATT 180
Db 1531 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGACATGATTTGGACGAACCACTAAATT 1590
Qy 181 CCGCATTCGACAGAT-ATTGPTATTAAGTGCCTAGCTCGATACAAATAAACCCCATTTGAC 239
Db 1591 CCGCATTCGACAGATAATTGTTATTAAGTGCCTAGCTCGATACAAATAAACCCCATTTGAC 1650
Qy 240 CATTCCACCATTTGGTGTGCACCTC 264
Db 1651 CATTCCACCATTTGGTGTGCACCTC 1675

RESULT 39

US-09-484-996-23
; Sequence 23, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-23

Query Match 94.0%; Score 248.2; DB 4; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.9e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTTAAGCATGATGATTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTTAAGCATGATGATTTAGCAACA 1470
Qy 61 TGCCTTACAAGAGAGAAAGAACCCGTCATGCCGATTTGGTGAAGTAAGTGTACGA 120
Db 1471 TGCCTTACAAGAGAGAAAGAACCCGTCATGCCGATTTGGTGAAGTAAGTGTACGA 1530
Qy 121 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGACATGATTTGGACGAACCACTAAATT 180
Db 1531 TCGTGCCTTTATTAGGAAGCAACAGACGGGTCTGACATGATTTGGACGAACCACTAAATT 1590
Qy 181 CCGCATTCGACAGAT-ATTGPTATTAAGTGCCTAGCTCGATACAAATAAACCCCATTTGAC 239
Db 1591 CCGCATTCGACAGATAATTGTTATTAAGTGCCTAGCTCGATACAAATAAACCCCATTTGAC 1650
Qy 240 CATTCCACCATTTGGTGTGCACCTC 264
Db 1651 CATTCCACCATTTGGTGTGCACCTC 1675

RESULT 40

US-09-484-996-28
; Sequence 28, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H

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RESULT 42
US-09-479-123-23
; Sequence 23, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:

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Qy 181 CCGCATTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACATAAATGCGCATTTGAC 239
Db 1725 CCGCATTGCAGAGATAATTGTAATTTAAGTGCCTAGCTCGATACATAAATGCGCATTTGAC 1784
Qy 240 CATTCAACACATTTGGTGTGCACCTC 264
Db 1785 CATTCAACACATTTGGTGTGCACCTC 1809

RESULT 45

US-09-484-997-24
; Sequence 24, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-24

Query Match 94.0%; Score 248.2; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db 1545 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1604
Qy 61 TGCCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTAAGTGGTGTACGA 120
Db 1605 TGCCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTAAGTGGTGTACGA 1664
Qy 121 TCGTCCCTTTATTAGGAAGCAGACAGCGGTCTGACATGGATTTGGAGCAACCACTAAATT 180
Db 1665 TCGTCCCTTTATTAGGAAGCAGACAGCGGTCTGACATGGATTTGGAGCAACCACTAAATT 1724
Qy 181 CCGCATTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACATAAATGCGCATTTGAC 239
Db 1725 CCGCATTGCAGAGATAATTGTAATTTAAGTGCCTAGCTCGATACATAAATGCGCATTTGAC 1784
Qy 240 CATTCAACACATTTGGTGTGCACCTC 264
Db 1785 CATTCAACACATTTGGTGTGCACCTC 1809

RESULT 46

US-09-481-355-24
; Sequence 24, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-24

Query Match 94.0%; Score 248.2; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db 1545 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1604
Qy 61 TGCCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTAAGTGGTGTACGA 120
Db 1605 TGCCTTACAGGAGAGAAAAGCACCCTGATGCCGATTTGGTAAGTGGTGTACGA 1664
Qy 121 TCGTCCCTTTATTAGGAAGCAGACAGCGGTCTGACATGGATTTGGAGCAACCACTAAATT 180
Db 1665 TCGTCCCTTTATTAGGAAGCAGACAGCGGTCTGACATGGATTTGGAGCAACCACTAAATT 1724
Qy 181 CCGCATTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATACATAAATGCGCATTTGAC 239
Db 1725 CCGCATTGCAGAGATAATTGTAATTTAAGTGCCTAGCTCGATACATAAATGCGCATTTGAC 1784
Qy 240 CATTCAACACATTTGGTGTGCACCTC 264
Db 1785 CATTCAACACATTTGGTGTGCACCTC 1809

RESULT 47

US-09-481-282-24
; Sequence 24, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US

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; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-24

Query Match          94.0%; Score 248.2; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      1  AATGTAGTCTTATGCAATACACTCTCTTAGTCTTTGCAACATGTGTAAAGATGTAGTGTAGCAACA 60
Db      1545  AATGTAGTCTTATGCAATACACTCTCTTAGTCTTTGCAACATGTGTAAAGATGTAGTGTAGCAACA 1604

QY      61  TGCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAAGGTGGTACGA 120
Db      1605  TGCCTTACAGGAGAGAAAAGACACCGTGCATGCCGATTGGTGGAAAGTAAAGGTGGTACGA 1664

QY      121  TGTGCGCTTATTAGGAAGGCAACAGACGGGTCTGACATGATGTGACGCAACCACTAAATT 180
Db      1665  TGTGCGCTTATTAGGAAGGCAACAGACGGGTCTGACATGATGTGACGCAACCACTAAATT 1724

QY      181  CGSCATTGCAGAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATATAAGCCCATTTGCAC 239
Db      1725  CGSCATTGCAGAGATATTGTATTTAAGTGGCTAGCTCGATACATATAAGCCCATTTGCAC 1784

QY      240  CATTCAACACATTGGTGTGCACCTC 264
Db      1785  CATTCAACACATTGGTGTGCACCTC 1809

RESULT 49
US-09-484-996-24
; Sequence 24, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHEPFF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base

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LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-24

Query Match 94.0%; Score 248.2; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db 1545 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1604
QY 61 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 120
Db 1605 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 1664
QY 121 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 180
Db 1665 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 1724
QY 181 CGCATTTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATGATGGAACCAACCACTAAATT 239
Db 1725 CGCATTTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATGATGGAACCAACCACTAAATT 1784
QY 240 CATTCACCAATTTGGTGTGCACCTC 264
Db 1785 CATTCACCAATTTGGTGTGCACCTC 1809

RESULT 50
US-09-479-123-24
; Sequence 24, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-24

Query Match 94.0%; Score 248.2; DB 4; Length 9871;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db 1545 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1604
QY 61 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 120
Db 1605 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 1664
QY 121 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 180
Db 1665 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 1724
QY 181 CGCATTTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATGATGGAACCAACCACTAAATT 239
Db 1725 CGCATTTGCAGAGAT-ATTGTAATTTAAGTGCCTAGCTCGATGATGGAACCAACCACTAAATT 1784
QY 240 CATTCACCAATTTGGTGTGCACCTC 264
Db 1785 CATTCACCAATTTGGTGTGCACCTC 1809

RESULT 51
US-09-479-122-25
; Sequence 25, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-25

Query Match 94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
Db 1734 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 1793
QY 61 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 120
Db 1794 TGCCTTACAAGGAGAGAAAAGCAACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 1853
QY 121 TCGTGCCTTATTAGGAAGCAACACCGTGCATGCCGATTTGGTGAAGTAAAGTGGTACGA 180

Db 1854 TCGTGCCCTTATTAGGAGGCAACAGACAGGCTGTGACATGGATTGGACCAACCACTGAATT 1913
QY 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATTTCAC 239
Db 1914 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATTTCAC 1973
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1974 CATTACCAACATTTGGTGTGCACCTC 1998

RESULT 52

US-09-484-997-25
; Sequence 25, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25

; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-25

Query Match 94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGCTTTATGCAATACCTCTTTAGTCTTGGCAATGTAACGATGATGAGCAACA 60
Db 1734 AATGTAGCTTTATGCAATACCTCTTTAGTCTTGGCAATGTAACGATGATGAGCAACA 1793
QY 61 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTGGTGGAAAGTAAGGTGTACGA 120
Db 1794 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTGGTGGAAAGTAAGGTGTACGA 1853
QY 121 TCGTGCCCTTATTAGGAGGCAACAGACCGGTCTGCATGGATTGGACCAACCACTAAATT 180
Db 1854 TCGTGCCCTTATTAGGAGGCAACAGACCGGTCTGCATGGATTGGACCAACCACTAAATT 1913
QY 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATTTCAC 239
Db 1914 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATTTCAC 1973
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1974 CATTACCAACATTTGGTGTGCACCTC 1998

Query Match 94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGCTTTATGCAATACCTCTTTAGTCTTGGCAATGTAACGATGATGAGCAACA 60
Db 1734 AATGTAGCTTTATGCAATACCTCTTTAGTCTTGGCAATGTAACGATGATGAGCAACA 1793
QY 61 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTGGTGGAAAGTAAGGTGTACGA 120
Db 1794 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTGGTGGAAAGTAAGGTGTACGA 1853
QY 121 TCGTGCCCTTATTAGGAGGCAACAGACCGGTCTGCATGGATTGGACCAACCACTAAATT 180
Db 1854 TCGTGCCCTTATTAGGAGGCAACAGACCGGTCTGCATGGATTGGACCAACCACTAAATT 1913
QY 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATTTCAC 239
Db 1914 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATTTCAC 1973
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1974 CATTACCAACATTTGGTGTGCACCTC 1998

RESULT 53

US-09-481-355-25
; Sequence 25, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25

; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-25

Query Match 94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 1 AATGTAGCTTTATGCAATACCTCTTTAGTCTTGGCAATGTAACGATGATGAGCAACA 60
Db 1734 AATGTAGCTTTATGCAATACCTCTTTAGTCTTGGCAATGTAACGATGATGAGCAACA 1793
QY 61 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTGGTGGAAAGTAAGGTGTACGA 120
Db 1794 TGCCTTACAGGAGAGAAAAGACCGCTGCATGCCGATTGGTGGAAAGTAAGGTGTACGA 1853
QY 121 TCGTGCCCTTATTAGGAGGCAACAGACCGGTCTGCATGGATTGGACCAACCACTAAATT 180
Db 1854 TCGTGCCCTTATTAGGAGGCAACAGACCGGTCTGCATGGATTGGACCAACCACTAAATT 1913
QY 181 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATTTCAC 239
Db 1914 CGCATTGCGAGAGAT-ATTGTATTAAAGTGCCTAGCTCGATACAAATAAAGCCATTTCAC 1973
QY 240 CATTACCAACATTTGGTGTGCACCTC 264
Db 1974 CATTACCAACATTTGGTGTGCACCTC 1998

RESULT 54

US-09-481-282-25
; Sequence 25, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

```
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-481-282-25

Query Match          94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTTGCAACATGTTAGCAACA 60
Db 1734 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTTGCAACATGTTAGCAACA 1793

QY 61 TGCTTACAGGAGAGAAAAGCACCGTGCATCGCATGTTGGTGAAGTAAAGTGGTACGA 120
Db 1794 TGCTTACAGGAGAGAAAAGCACCGTGCATCGCATGTTGGTGAAGTAAAGTGGTACGA 1853

QY 121 TGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 180
Db 1854 TGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 1913

QY 181 CGCGATTCGACAGAT-ATTGTATTATTAGTGCCTAGCTAGTACATCAATAAAGCCATTGAC 239
Db 1914 CGCGATTCGACAGATATTGTATTATTAGTGCCTAGCTAGTACATCAATAAAGCCATTGAC 1973

QY 240 CATTCCACCATTTGGTGTGCACCTC 264
Db 1974 CATTCCACCATTTGGTGTGCACCTC 1998

RESULT 55
US-09-455-659A-25
; Sequence 25, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
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; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/481,223
; CURRENT FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-455-659A-25

Query Match          94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTTGCAACATGTTAGCAACA 60
Db 1734 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTTGCAACATGTTAGCAACA 1793

QY 61 TGCTTACAGGAGAGAAAAGCACCGTGCATCGCATGTTGGTGAAGTAAAGTGGTACGA 120
Db 1794 TGCTTACAGGAGAGAAAAGCACCGTGCATCGCATGTTGGTGAAGTAAAGTGGTACGA 1853

QY 121 TGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 180
Db 1854 TGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATT 1913

QY 181 CGCGATTCGACAGAT-ATTGTATTATTAGTGCCTAGCTAGTACATCAATAAAGCCATTGAC 239
Db 1914 CGCGATTCGACAGATATTGTATTATTAGTGCCTAGCTAGTACATCAATAAAGCCATTGAC 1973

QY 240 CATTCCACCATTTGGTGTGCACCTC 264
Db 1974 CATTCCACCATTTGGTGTGCACCTC 1998

RESULT 56
US-09-484-996-25
; Sequence 25, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
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```

; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-998-25

Query Match      94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAAGTGTAGGTAACA 60
Db 1734 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAAGTGTAGGTAACA 1793
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGTTGCGAAGTAAAGTGTACGA 120
Db 1794 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGTTGCGAAGTAAAGTGTACGA 1853
QY 121 TCGTGCCCTTATTAGGAAGCAACAGACCGGTGTCATGCGGTTGCGAAGTAAAGTGTACGA 180
Db 1854 TCGTGCCCTTATTAGGAAGCAACAGACCGGTGTCATGCGGTTGCGAAGTAAAGTGTACGA 1913
QY 181 CGCATTCACAGAGAT-ATTGTATTAAAGTGCCTAGCTGATACATAAATTAAGTGCCTAGC 239
Db 1914 CGCATTCACAGAGAT-ATTGTATTAAAGTGCCTAGCTGATACATAAATTAAGTGCCTAGC 1973
QY 240 CATTCCACACATTTGGTGTGCACCTC 264
Db 1974 CATTCCACACATTTGGTGTGCACCTC 1998

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RESULT 57
US-09-479-123-25
; Sequence 25, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-25

Query Match      94.0%; Score 248.2; DB 4; Length 10060;
Best Local Similarity 98.5%; Pred. No. 2e-77;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAAGTGTAGGTAACA 60
Db 1734 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAAGTGTAGGTAACA 1793
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGTTGCGAAGTAAAGTGTACGA 120
Db 1794 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGTTGCGAAGTAAAGTGTACGA 1853
QY 121 TCGTGCCCTTATTAGGAAGCAACAGACCGGTGTCATGCGGTTGCGAAGTAAAGTGTACGA 180
Db 1854 TCGTGCCCTTATTAGGAAGCAACAGACCGGTGTCATGCGGTTGCGAAGTAAAGTGTACGA 1913
QY 181 CGCATTCACAGAGAT-ATTGTATTAAAGTGCCTAGCTGATACATAAATTAAGTGCCTAGC 239
Db 1914 CGCATTCACAGAGAT-ATTGTATTAAAGTGCCTAGCTGATACATAAATTAAGTGCCTAGC 1973
QY 240 CATTCCACACATTTGGTGTGCACCTC 264
Db 1974 CATTCCACACATTTGGTGTGCACCTC 1998

RESULT 58
US-09-167-322-13
; Sequence 13, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 13:
; LENGTH: 565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-167-322-13

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Query Match      92.7%; Score 244.8; DB 4; Length 565;
Best Local Similarity 97.4%; Pred. No. 8.8e-77;
Matches 261; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATG-----GTAACGATGATGTAG 55

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Db 233 ATGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGCTTATGATGATGAGTTAG 292
QY 56 CAACATGCTTACAGAGAGAGAAAAGACCGTGCATGCCGATTTGGTGGAGATGAGTGG 115
Db 293 CAACATGCTTACAGAGAGAGAAAAGACCGTGCATGCCGATTTGGTGGAGATGAGTGG 352
QY 116 TAGCATGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACT 175
Db 353 TAGCATGCTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACT 412
QY 176 AAATTCCGCAATTCGACAGATATTGATTAAAGTCCGCTAGCTCGCATCAATAAAGCCCAAT 235
Db 413 GAATTCGCGCAATTCGACAGATATTGATTAAAGTCCGCTAGCTCGCATCAATAAAGCCCAAT 472
QY 236 TGACCAATTCACCAATTCGATGCTGCACT 263
Db 473 TGACCAATTCACCAATTCGATGCTGCACT 500

RESULT 59
US-08-972-218-2
; Sequence 2, Application US/08972218
; Patent No. 6197502
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Oberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.
; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE
; TITLE OF INVENTION: DISCOVERY, CHARACTERIZATION AND ISOLATION OF GENES
; TITLE OF INVENTION: ENCODING POLYPEPTIDES WITH A PREDETERMINED PROPERTY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of The Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,218
; FILING DATE: 14-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 008358-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5656
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9521 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-972-218-2

Query Match 77.7%; Score 205.2; DB 3; Length 9521;
Best Local Similarity 98.6%; Pred. No. 3e-62;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGCTTATGATGATGAGTTAGCAACAT 61

Db 664 ATCCAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGCTTATGATGATGAGTTAGCAACAT 723
QY 62 GCCTTACAGGAGAGAGAAAAGACCGTGCATGCCGATTTGGTGGAGATGAGTGGTACGAT 121
Db 724 GCCTTACAGGAGAGAGAAAAGACCGTGCATGCCGATTTGGTGGAGATGAGTGGTACGAT 783
QY 122 CGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATTC 181
Db 784 CGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATTC 843
QY 182 CGCATTCGAGAGATATTGATTAAAGTGCC 211
Db 844 CGCATTCGAGAGATATTGATTAAAGTGCC 873

RESULT 60
US-09-193-707-2
; Sequence 2, Application US/09193707
; Patent No. 6524792
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Oberger, Georg H.
; APPLICANT: Koller, Daniel
; APPLICANT: Bailey, James E.
; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY,
; TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WITH
; TITLE OF INVENTION: A PREDETERMINED PROPERTY
; FILE REFERENCE: 8358-0005-999
; CURRENT APPLICATION NUMBER: US/09/193,707
; CURRENT FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 9521
; TYPE: DNA
; ORGANISM: Alphavirus, Sindbis Virus
US-09-193-707-2

Query Match 77.7%; Score 205.2; DB 4; Length 9521;
Best Local Similarity 98.6%; Pred. No. 3e-62;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGTAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGCTTATGATGATGAGTTAGCAACAT 61
Db 664 ATCCAGTCTTATGCAATACCTCTTGTAGTCTTGTGCAATGCTTATGATGATGAGTTAGCAACAT 723
QY 62 GCCTTACAGGAGAGAGAAAAGACCGTGCATGCCGATTTGGTGGAGATGAGTGGTACGAT 121
Db 724 GCCTTACAGGAGAGAGAAAAGACCGTGCATGCCGATTTGGTGGAGATGAGTGGTACGAT 783
QY 122 CGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATTC 181
Db 784 CGTGCTTATTAGGAGGCAACAGACGGGTCTGACATGGATTGGACGACCACTAAATTC 843
QY 182 CGCATTCGAGAGATATTGATTAAAGTGCC 211
Db 844 CGCATTCGAGAGATATTGATTAAAGTGCC 873

RESULT 61
US-09-733-042-1
; Sequence 1, Application US/09733042
; Patent No. 6576443
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10

	Query Match	29.2%	Score 77;	DB 1;	Length 6926;
	Best Local Similarity	98.9%;	Pred. No. 5.1e-17;		
	Matches	88;	Conservative	0;	Mismatches 0; Indels 1; Gaps 1;
QY	177	AATTCGGCATTGCAGAGAT-ATTGTATTTAAGTCGCTGAGTCGATACAAATAACGCCATT	235		
Db	683	AATTCGGCATTGCAGAGATAATTGTTTAAAGTCGCTGAGTCGATACAAATAACGCCATT	742		
QY	236	TGAGCATTTACACACATTGGGTGCACCTC	264		
Db	743	TGAGCATTTACACACATTGGGTGCACCTC	771		

RESULT 63
US-09-299-141-5
; Sequence 5, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG J.
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY

```

/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 7492
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
US-09-299-141-5

Query Match          29.2%;      Score 77;  DB 4;  Length 7492;
Best Local Similarity 98.9%;    Pred NO. 5.3e-17;
Matches 88;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

QY      177  AATTCGCGATTGCAGAGAT-ATTGTAATTAAAGTCCTAGCTCGATACAAATAACGCCATT 235
Db      1    AATTCGCGATTGCAGAGATAATTGTAATTAAAGTCCTAGCTCGATACAAATAACGCCATT 60

QY      236  TGACCAATTACCAACATTGGTGTGCACCTC 264
Db      61  TGACCAATTACCAACATTGGTGTGCACCTC 89

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RESULT 64
US-08-989-394-10
; Sequence 10, Application US/08989394
; Patent No. 5994136
;
GENERAL INFORMATION:
;
; APPLICANT: Maldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
;
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; TITLE OF INVENTION: TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
;
NUMBER OF SEQUENCES: 22
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPRAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,394
FILING DATE: 12-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-989-394-10

Query Match 19.6%; Score 51.8; DB 2; Length 74;
Best Local Similarity 96.4%; Pred. No. 5.5e-09;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 176 AAATTCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 230
|||
Db 1 AATTGCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 55
|||

RESULT 65
US-09-271-365-10
Sequence 10, Application US/09271365
Patent No. 6165782
GENERAL INFORMATION:
APPLICANT: Naldini, Luigi
Dull, Thomas
Farson, Deborah A.
Witt, Rochelle
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPHEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-271-365-10

Query Match 19.6%; Score 51.8; DB 3; Length 74;
Best Local Similarity 96.4%; Pred. No. 5.5e-09;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 176 AAATTCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 230
|||
Db 1 AATTGCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 55
|||

RESULT 66
US-09-604-013A-10
Sequence 10, Application US/09604013A
Patent No. 6428953
GENERAL INFORMATION:
APPLICANT: Naldini, Luigi
Dull, Thomas
Farson, Deborah A.
Witt, Rochelle
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPHEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/604,013A
FILING DATE: 26-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-604-013A-10

Query Match 19.6%; Score 51.8; DB 4; Length 74;
Best Local Similarity 96.4%; Pred. No. 5.5e-09;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 176 AAATTCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 230
|||
Db 1 AATTGCGCGATTGCGAGATATTGTTTAAAGTGGCTAGCTCGATACATAAAGC 55
|||

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RESULT 67
US-08-989-394-11/c
; Sequence 11, Application US/08989394
; Patent No. 5994136
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,394
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7860
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; APPLICATION NUMBER: US/08/989,394
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7860
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-989-394-11

Query Match 18.9%; Score 50; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTGATACATAAAGC 230
Db 73 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTGATACATAAAGC 24

RESULT 68
US-09-271-365-11/c
; Sequence 11, Application US/09271365
; Patent No. 6165782
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/604,013A
; FILING DATE: 26-JUN-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-271-365-11

Query Match 18.9%; Score 50; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 181 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTGATACATAAAGC 230
Db 73 CGCATTGCAGAGATATTGTTTAAAGTCCCTAGCTGATACATAAAGC 24

RESULT 69
US-09-604-013A-11/c
; Sequence 11, Application US/09604013A
; Patent No. 6428953
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/604,013A
; FILING DATE: 26-JUN-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.

```

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;
;   REGISTRATION NUMBER: 33,981
;   REFERENCE/DOCKET NUMBER: A7086
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202)293-7060
;   TELEFAX: (202)293-7860
;   INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 74 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-604-013A-11

Query Match      18.9%; Score 50; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  181 CGCATTGCAGAGATATTGTTTAAAGTGCGCTAGCTCGATACATAAAGC 230
DB  73 CGCATTGCAGAGATATTGTTTAAAGTGCGCTAGCTCGATACATAAAGC 24

RESULT 70
US-08-272-513-1
; Sequence 1, Application US/08272513
; Patent No. 5558867
; GENERAL INFORMATION:
; APPLICANT: Sakaguchi, Masashi
; APPLICANT: Yamamoto, Michitaka
; TITLE OF INVENTION: RECOMBINANT MAREK'S DISEASE VIRUS,
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME AND VACCINE CONTAINING THE
; TITLE OF INVENTION: SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,513
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,554
; FILING DATE: 08-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-500-23477
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-0400
; TELEFAX: 202-835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3001 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Marek's disease gammaherpesvirus
; STRAIN: 61-554 and BC-1
US-08-272-513-1
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Query Match      17.0%; Score 44.8; DB 1; Length 3001;
Best Local Similarity 81.2%; Pred. No. 8.3e-06;
Matches 52; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY  200 TATTTAAGTGCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTC 259
DB  2108 TATATAAGCTGTTGCCACCATCAATAAAGCCATTTCACCATTCACCATTCGTC 2167

QY  260 ACCT 263
DB  2168 ACCT 2171

RESULT 71
US-08-379-452-9/c
; Sequence 9, Application US/08379452
; Patent No. 6040174
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; TITLE OF INVENTION: COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,452
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (ONG5893)
US-08-379-452-9

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  231 CCATTGACATTTCACCATTCGTCGACCT 263
DB  47 CCATTGACATTTCACCATTCGTCGACCT 15

RESULT 72
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US-08-682-794-5/c
; Sequence 5, Application US/08682794
; Patent No. 6110735
; GENERAL INFORMATION:
; APPLICANT: CILE CHARTIER et al.
; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/08/682,794
; CURRENT FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-08-682-794-5

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 CCATTGACCATTCACCATTCGTTGTGCACCT 263
Db 47 CCATTGACCATTCACCATTCGTTGTGCACCT 15

RESULT 73
US-09-409-670-9/c
; Sequence 9, Application US/09409670
; Patent No. 6133028
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Iuoc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANT, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/09/467,952
; EARLIER FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 08/682,794
; EARLIER FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-09-409-670-9-5

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 CCATTGACCATTCACCATTCGTTGTGCACCT 263
Db 47 CCATTGACCATTCACCATTCGTTGTGCACCT 15

RESULT 74
US-09-467-952-5/c
; Sequence 5, Application US/09467952
; Patent No. 6281000
; GENERAL INFORMATION:
; APPLICANT: CILE CHARTIER et al.
; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/09/467,952
; EARLIER FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 08/682,794
; EARLIER FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-09-467-952-5

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 CCATTGACCATTCACCATTCGTTGTGCACCT 263
Db 47 CCATTGACCATTCACCATTCGTTGTGCACCT 15

RESULT 75
US-09-167-322-10
; Sequence 10, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel,
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Padio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

```

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; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
US-09-409-670-9

Query Match      12.5%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 CCATTGACCATTCACCATTCGTTGTGCACCT 263
Db 47 CCATTGACCATTCACCATTCGTTGTGCACCT 15

RESULT 76
US-09-167-322-10
; Sequence 10, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel,
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Padio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

```

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;
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1897 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-167-322-10

Query Match          11.9%; Score 31.4; DB 4; Length 1897;
Best Local Similarity 75.4%; Pred. No. 0.37;
Matches 52; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 196 ATTGATTAAAGTGCTAGCTCGATACATATAA-CGCCATTGTGACCATTCACCACTTGG 254
Db 1748 AATGTACTTAAGCTTGTGTGCTAACAATAAAGTGCCTTCTACCTCTCACCACTTGG 1807

QY 255 TGTGCACCT 263
Db 1808 TGTGCACCT 1816

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Search completed: March 11, 2004, 11:10:00
Job time : 56.7624 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 08:24:22 ; Search time 191.633 Seconds
(without alignments)
5071.893 Million cell updates/sec

Title: US-09-733-368a-1_COPY_349_612

Perfect score: 264

Sequence: 1 aatgtattatgaataac.....accacattgtgtgacatc 264

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Gapop 10.0 , Gapext 1.0

Searched: 2432557 seqs, 184079884 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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12: /cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	262.4	99.4	8238	10	US-09-482-682-50
2	262.4	99.4	33622	15	US-10-403-337-44
3	262.4	99.4	33622	15	US-10-351-890-44
4	262.4	99.4	35211	15	US-10-403-337-43
5	262.4	99.4	35211	15	US-10-351-890-43
6	257.2	97.4	262	9	US-09-965-703-69
7	257.2	97.4	262	12	US-10-239-134-61
8	248.2	94.0	6836	14	US-10-331-329-18
9	248.2	94.0	8902	9	US-09-729-416A-1
10	248.2	94.0	9737	14	US-10-331-329-22
11	248.2	94.0	9737	14	US-10-331-329-23
12	248.2	94.0	9737	14	US-10-331-329-28
13	248.2	94.0	9871	14	US-10-331-329-24
14	248.2	94.0	10060	14	US-10-331-329-25
15	248.2	94.0	11265	14	US-10-185-799-1

16	248.2	94.0	11265	14	US-10-185-799-1	Sequence 1, Appli
17	232	87.9	5130	9	US-09-897-006-9	Sequence 9, Appli
18	232	87.9	5130	10	US-09-897-511A-9	Sequence 9, Appli
19	217.4	82.3	10469	14	US-10-155-736A-1	Sequence 1, Appli
20	205.2	77.7	11282	9	US-09-733-042-1	Sequence 1, Appli
21	205.2	77.7	11282	10	US-09-275-883-1	Sequence 1, Appli
22	187.6	71.1	5283	11	US-09-921-143-36	Sequence 36, Appl
23	174.2	66.0	6250	12	US-10-182-327-16	Sequence 16, Appl
24	174.2	66.0	6250	15	US-10-182-329-109	Sequence 109, App
25	173.4	65.7	11600	9	US-09-847-101B-35	Sequence 35, Appl
26	173.4	65.7	11600	10	US-09-482-682-49	Sequence 49, Appl
27	173.4	65.7	11600	15	US-10-403-337-42	Sequence 42, Appl
28	173.4	65.7	11600	15	US-10-351-890-42	Sequence 42, Appl
29	171.8	65.1	6279	15	US-10-182-329-1	Sequence 1, Appli
30	171.8	65.1	8513	15	US-10-182-329-9	Sequence 9, Appli
31	161.2	61.1	786	15	US-10-264-237-633	Sequence 633, App
32	77	29.2	7492	14	US-10-267-117-5	Sequence 5, Appli
33	77	29.2	7492	14	US-10-340-112-5	Sequence 5, Appli
34	51.8	19.6	74	13	US-10-192-085-10	Sequence 10, Appl
35	50	18.9	74	13	US-10-192-085-11	Sequence 11, Appl
36	33	12.5	47	9	US-09-725-720-9	Sequence 9, Appli
37	33	12.5	47	9	US-09-938-491-5	Sequence 5, Appli
38	33	12.5	47	10	US-09-739-007-9	Sequence 9, Appli
39	33	12.5	542	15	US-10-027-632-81543	Sequence 81543, A
40	33	12.5	542	15	US-10-027-632-301875	Sequence 301875, A
41	33	12.5	573	15	US-10-027-632-50648	Sequence 50648, A
42	32.2	12.2	2877	15	US-10-369-493-25133	Sequence 25133, A
43	31.4	11.9	669	12	US-10-424-599-52313	Sequence 52313, A
44	31	11.7	595	12	US-10-424-599-132712	Sequence 132712, A
45	30.8	11.7	1330	12	US-10-424-599-14875	Sequence 14875, A
46	30.8	11.7	2664	15	US-10-027-632-112120	Sequence 112120, A
47	30.6	11.6	5214	15	US-10-027-632-175173	Sequence 175173, A
48	30.4	11.5	3300	12	US-10-425-114-31887	Sequence 31887, A
49	30.2	11.4	1202	9	US-09-739-254-63	Sequence 63, Appl
50	30.2	11.4	1202	9	US-09-904-615-63	Sequence 63, Appl
51	30.2	11.4	1202	14	US-10-054-988-63	Sequence 63, Appl
52	30.2	11.4	1202	14	US-10-055-988-63	Sequence 63, Appl
53	30.2	11.4	1452	9	US-09-739-254-34	Sequence 34, Appl
54	30.2	11.4	1452	9	US-09-904-615-34	Sequence 34, Appl
55	30.2	11.4	1452	14	US-10-054-988-34	Sequence 34, Appl
56	30.2	11.4	1452	14	US-10-055-988-34	Sequence 34, Appl
57	30	11.4	834	15	US-10-027-632-165752	Sequence 165752, A
58	30	11.4	834	15	US-10-027-632-165753	Sequence 165753, A
59	29.6	11.2	2271	15	US-10-398-221-1044	Sequence 1044, Ap
60	29.6	11.2	2271	15	US-10-398-221-2861	Sequence 2861, Ap
61	29.6	11.2	302250	9	US-09-962-832-154	Sequence 154, App
62	29.2	11.1	183	15	US-10-027-632-63861	Sequence 63861, A
63	29.2	11.1	637	15	US-10-027-632-64765	Sequence 64765, A
64	29.2	11.1	752	15	US-10-027-632-63862	Sequence 63862, A
65	29.2	11.1	752	15	US-10-027-632-64766	Sequence 64766, A
66	29.2	11.1	752	15	US-10-027-632-310455	Sequence 310455, A
67	29.2	11.1	752	15	US-10-027-632-310456	Sequence 310456, A
68	29.2	11.1	5297	14	US-10-027-632-35424	Sequence 35424, A
69	29.2	11.1	5297	14	US-10-311-455-820	Sequence 820, App
70	29.2	11.1	5297	16	US-10-257-166-84	Sequence 84, Appl
71	29	11.0	518	12	US-10-424-599-17797	Sequence 17797, A
72	29	11.0	1438	9	US-09-764-847-1659	Sequence 1659, Ap
73	29	11.0	1438	14	US-10-092-154-1659	Sequence 1659, Ap
74	29	11.0	3208	15	US-10-220-891-5	Sequence 5, Appli
75	29	11.0	6102	14	US-10-097-534-5	Sequence 5, Appli
76	29	11.0	6396	14	US-10-037-270-226	Sequence 226, App
77	29	11.0	6396	15	US-10-117-722-226	Sequence 226, App
78	29	11.0	7515	9	US-09-070-927A-28	Sequence 28, Appl
79	28.8	10.9	577	9	US-09-796-692-6990	Sequence 6990, Ap
80	28.8	10.9	577	14	US-10-040-862-6990	Sequence 6990, Ap
81	28.8	10.9	577	15	US-10-057-475B-6990	Sequence 6990, Ap
82	28.8	10.9	577	15	US-10-154-884B-6990	Sequence 6990, Ap
83	28.8	10.9	790	15	US-10-027-632-325190	Sequence 325190, A
84	28.8	10.9	841	15	US-10-027-632-103849	Sequence 103849, A
85	28.8	10.9	841	15	US-10-027-632-323564	Sequence 323564, A
86	28.8	10.9	2908	15	US-10-369-493-46299	Sequence 46299, A
87	28.6	10.8	676	15	US-10-027-632-134758	Sequence 134758, A
88	28.6	10.8	676	15	US-10-027-632-134759	Sequence 134759, A

US-10-351-890-44

Query Match 99.4%; Score 262.4; DB 15; Length 3521;
Best Local Similarity 99.6%; Pred. No. 2.7e-79;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCTTATGCAATCTCTTTAGTCTTGGCAATGCTAAGCATGAGTTAGCAACA 60
DB 533 AATGAGCTTATGCAATCTCTTTAGTCTTGGCAATGCTAAGCATGAGTTAGCAACA 592
QY 61 TGCCTTACAGAGGAGAAAGACCGTGCATGCCGATTTGGTGAAGTAAAGTTAGGTACGA 120
DB 593 TGCCTTACAGAGGAGAAAGACCGTGCATGCCGATTTGGTGAAGTAAAGTTAGGTACGA 652
QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGAGTAAAGTAAAT 180
DB 653 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGAGTAAAGTAAAT 712
QY 181 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 240
DB 713 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 772
QY 241 ATTCAACACATTTGGTGCACCTC 264
DB 773 ATTCAACACATTTGGTGCACCTC 796

RESULT 4

US-10-403-337-43

; Sequence 43, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; PRIOR FILING DATE: 2003-03-27
; PRIOR FILING DATE: 2003-01-24
; PRIOR FILING DATE: 2003-01-24
; PRIOR FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid AvinBg

Query Match 99.4%; Score 262.4; DB 15; Length 3521;
Best Local Similarity 99.6%; Pred. No. 2.7e-79;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCTTATGCAATCTCTTTAGTCTTGGCAATGCTAAGCATGAGTTAGCAACA 60
DB 647 AATGAGCTTATGCAATCTCTTTAGTCTTGGCAATGCTAAGCATGAGTTAGCAACA 706
QY 61 TGCCTTACAGAGGAGAAAGACCGTGCATGCCGATTTGGTGAAGTAAAGTTAGGTACGA 120
DB 707 TGCCTTACAGAGGAGAAAGACCGTGCATGCCGATTTGGTGAAGTAAAGTTAGGTACGA 766
QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGAGTAAAGTAAAT 180
DB 767 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGAGTAAAGTAAAT 826
QY 181 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 240
DB 773 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 796

RESULT 5

US-10-351-890-43

; Sequence 43, Application US/10351890
; Publication No. US2004002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid AvinBg

Query Match 99.4%; Score 262.4; DB 15; Length 3521;
Best Local Similarity 99.6%; Pred. No. 2.7e-79;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCTTATGCAATCTCTTTAGTCTTGGCAATGCTAAGCATGAGTTAGCAACA 60
DB 647 AATGAGCTTATGCAATCTCTTTAGTCTTGGCAATGCTAAGCATGAGTTAGCAACA 706
QY 61 TGCCTTACAGAGGAGAAAGACCGTGCATGCCGATTTGGTGAAGTAAAGTTAGGTACGA 120
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QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGAGTAAAGTAAAT 180
DB 767 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGAGTAAAGTAAAT 826
QY 181 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 240
DB 773 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 796

DB 827 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 886

QY 241 ATTCAACACATTTGGTGCACCTC 264

DB 887 ATTCAACACATTTGGTGCACCTC 910

RESULT 5

US-10-351-890-43

; Sequence 43, Application US/10351890
; Publication No. US2004002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid AvinBg

Query Match 99.4%; Score 262.4; DB 15; Length 3521;
Best Local Similarity 99.6%; Pred. No. 2.7e-79;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGAGCTTATGCAATCTCTTTAGTCTTGGCAATGCTAAGCATGAGTTAGCAACA 60
DB 647 AATGAGCTTATGCAATCTCTTTAGTCTTGGCAATGCTAAGCATGAGTTAGCAACA 706
QY 61 TGCCTTACAGAGGAGAAAGACCGTGCATGCCGATTTGGTGAAGTAAAGTTAGGTACGA 120
DB 707 TGCCTTACAGAGGAGAAAGACCGTGCATGCCGATTTGGTGAAGTAAAGTTAGGTACGA 766
QY 121 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGAGTAAAGTAAAT 180
DB 767 TCGTGCCTTATTAGGAAGCAACAGACGGGTCTGCATGCTGATGAGTAAAGTAAAT 826
QY 181 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 240
DB 827 CGCATTTGCAGAGATTTGATTTAAGTGCCTAGCTGCATACATTAAGCCATTGACC 886

RESULT 6

US-09-965-703-69

; Sequence 69, Application US/09965703
; Patent No. US20020119521A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20020119521A1e1 Bodysonic Receptor-Based Inducible Gene Expr
; FILE REFERENCE: A010203
; CURRENT APPLICATION NUMBER: US/09/965,703
; CURRENT FILING DATE: 2001-09-26


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; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/09050
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Rous sarcoma virus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: NO. US20020119521A1el Sequence
US-09-965-703-69

Query Match          97.4%; Score 257.2; DB 9; Length 262;
Best Local Similarity 98.9%; Pred. No. 1.7e-78;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGCTTAACGATGATGATGCAACAT 61
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QY 62 GCCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
DB 61 GCCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 122 CGTGCCTTATTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
DB 121 CGTGCCTTATTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 182 CGCATTCAGAGATATTTGATTAAAGTGCCCTAGCTCGATACATATAAAGCCATTTGACCA 241
DB 181 CGCATTCAGAGATATTTGATTAAAGTGCCCTAGCTCGATACATATAAAGCCATTTGACCA 240
QY 242 TTCACACATTTGGTGGACCT 263
DB 241 TTCACACATTTGGTGGACCT 262

RESULT 7
US-10-239-134-61
; Sequence 61, Application US/10239134
; Publication No. US20040033600A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; TITLE OF INVENTION: NO. US20040033600A1el Bodyeone Receptor-Based Inducible Gene Exp
; FILE REFERENCE: RH0020
; CURRENT APPLICATION NUMBER: US/10/239,134
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: NO. US20040033600A1el Sequence
US-10-239-134-61

Query Match          97.4%; Score 257.2; DB 12; Length 262;
Best Local Similarity 98.9%; Pred. No. 1.7e-78;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGCTTAACGATGATGATGCAACAT 61
DB 1 ATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGCTTAACGATGATGATGCAACAT 60
QY 62 GCCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
DB 61 GCCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 122 CGTGCCTTATTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
DB 121 CGTGCCTTATTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 182 CGCATTCAGAGATATTTGATTAAAGTGCCCTAGCTCGATACATATAAAGCCATTTGACCA 241
DB 181 CGCATTCAGAGATATTTGATTAAAGTGCCCTAGCTCGATACATATAAAGCCATTTGACCA 240
QY 242 TTCACACATTTGGTGGACCT 263
DB 241 TTCACACATTTGGTGGACCT 262

RESULT 8
US-10-331-329-18
; Sequence 18, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERFF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; CURRENT FILING DATE: 2002-12-30
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-331-329-18

Query Match          94.0%; Score 248.2; DB 14; Length 6836;
Best Local Similarity 98.5%; Pred. No. 1e-74; 3; Indels 1; Gaps 1;
Matches 261; Conservative 0; Mismatches 0;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGCTTAACGATGATGATGCAACAA 60
DB 1558 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGTGCAATGCTTAACGATGATGATGCAACAA 1617
QY 61 TGCCCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 1618 TGCCCTTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1677
QY 121 TCGTGCCTTATTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 1678 TCGTGCCTTATTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1737
QY 181 CGCATTCAGAGAT-ATTGTATTAAAGTGCCCTAGCTCGATACATATAAAGCCATTTGAC 239
DB 1738 CGCATTCAGAGATATTGTTATTAAAGTGCCCTAGCTCGATACATATAAAGCCATTTGAC 1797
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QY 240 CATTACCACATTTGGTGTGCACCTC 264
Db 1798 CATTACCACATTTGGTGTGCACCTC 1822

RESULT 9
US-09-729-416A-1
; Sequence 1, Application US/09729416A
; Patent No. US20020055172A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; TITLE OF INVENTION: MULTIPLE PROMOTER EXPRESSION CONSTRUCTS AND METHODS OF
; FILE REFERENCE: 0221-0004C
; CURRENT APPLICATION NUMBER: US/09/729,416A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8902
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: (PRIG-MPI)
US-09-729-416A-1

Query Match 94.0%; Score 248.2; DB 9; Length 8902;
Best Local Similarity 98.5%; Pred. No. 1.2e-74;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
Db 3624 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 3683

QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGAAGTGGTGTACGA 120
Db 3684 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGAAGTGGTGTACGA 3743

QY 121 TCGTGCCCTTATTAGGAAGCAACAGACGGGTCTGCATGATTTGGACGACCACTAAATT 180
Db 3744 TCGTGCCCTTATTAGGAAGCAACAGACGGGTCTGCATGATTTGGACGACCACTAAATT 3803

QY 181 CGCATTCGACAGAT-ATTGTATTAGTCCCTAGCTCGATACATAAAGCCATTGAC 239
Db 3804 CGCATTCGACAGAT-ATTGTATTAGTCCCTAGCTCGATACATAAAGCCATTGAC 3863

QY 240 CATTACCACATTTGGTGTGCACCTC 264
Db 3864 CATTACCACATTTGGTGTGCACCTC 3888

RESULT 10
US-10-331-329-22
; Sequence 22, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-22

Query Match 94.0%; Score 248.2; DB 14; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.2e-74;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
Db 1411 AATGTAGTCTTATGCAATCTCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGAAGTGGTGTACGA 120
Db 1471 TGCCTTACAGGAGAGAAAGACACCGTGCATGCCGATTGGTGAAGTGGTGTACGA 1530

QY 121 TCGTGCCCTTATTAGGAAGCAACAGACGGGTCTGCATGATTTGGACGACCACTAAATT 180
Db 1531 TCGTGCCCTTATTAGGAAGCAACAGACGGGTCTGCATGATTTGGACGACCACTAAATT 1590

QY 181 CGCATTCGACAGAT-ATTGTATTAGTCCCTAGCTCGATACATAAAGCCATTGAC 239
Db 1591 CGCATTCGACAGAT-ATTGTATTAGTCCCTAGCTCGATACATAAAGCCATTGAC 1650

QY 240 CATTACCACATTTGGTGTGCACCTC 264
Db 1651 CATTACCACATTTGGTGTGCACCTC 1675

RESULT 11
US-10-331-329-23
; Sequence 23, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
;
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-23

Query Match          94.0%; Score 248.2; DB 14; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.2e-74;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
DB 1411 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCGGATTCGTAAGTAAAGTGGTACGA 120
DB 1471 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCGGATTCGTAAGTAAAGTGGTACGA 1530

QY 121 TCGTGCCTTTATTAGGAGGCAACAGACAGGCTCTGACATGGATTCGTAAGTAAAGTGGTACGA 180
DB 1471 TCGTGCCTTTATTAGGAGGCAACAGACAGGCTCTGACATGGATTCGTAAGTAAAGTGGTACGA 1590

QY 181 CGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTGATACATAAAGCCACTTAC 239
DB 1591 CGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTGATACATAAAGCCACTTAC 1650

QY 240 CATTCAACACATTTGGTGTGCACCTC 264
DB 1651 CATTCAACACATTTGGTGTGCACCTC 1675

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RESULT 12
US-10-331-329-28
; Sequence 28, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10331,329
; PRIOR FILING DATE: 2002-12-30
; PRIOR FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1999-02-19
; PRIOR FILING DATE: 1998-09-24
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
;
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-28

```

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Query Match          94.0%; Score 248.2; DB 14; Length 9737;
Best Local Similarity 98.5%; Pred. No. 1.2e-74;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
DB 1411 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1470

QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCGGATTCGTAAGTAAAGTGGTACGA 120
DB 1471 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCGGATTCGTAAGTAAAGTGGTACGA 1530

QY 121 TCGTGCCTTTATTAGGAGGCAACAGACAGGCTCTGACATGGATTCGTAAGTAAAGTGGTACGA 180
DB 1531 TCGTGCCTTTATTAGGAGGCAACAGACAGGCTCTGACATGGATTCGTAAGTAAAGTGGTACGA 1590

QY 181 CGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTGATACATAAAGCCACTTAC 239
DB 1591 CGCATTCGACAGAT-ATTGTATTAAAGTGCCTAGCTGATACATAAAGCCACTTAC 1650

QY 240 CATTCAACACATTTGGTGTGCACCTC 264
DB 1651 CATTCAACACATTTGGTGTGCACCTC 1675

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RESULT 13
US-10-331-329-24
; Sequence 24, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10331,329
; PRIOR FILING DATE: 2002-12-30
; PRIOR FILING DATE: 1999-03-26
; PRIOR FILING DATE: 1999-03-08
; PRIOR FILING DATE: 1999-02-19
; PRIOR FILING DATE: 1998-09-24
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
;
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-24

Query Match          94.0%; Score 248.2; DB 14; Length 9871;
Best Local Similarity 98.5%; Pred. No. 1.2e-74;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 60
DB 1545 AATGTAGTCTTATGCAATACCTTGTAGTCTTGCACATGTAACGATGAGTTAGCAACA 1604

QY 61 TGCCTTACAAGGAGAGAAAAGCACCCTGTCATGCGGATTCGTAAGTAAAGTGGTACGA 120

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; PRIOR APPLICATION NUMBER: 09/402,020
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: PCT/AU98/00208
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: AU PP5891
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: AU P21830
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 11265
; ORGANISM: Murine
; US-10-155-736A-1
Query Match      94.0%; Score 248.2; DB 14; Length 11265;
Best Local Similarity 98.5%; Pred. No. 1.3e-74;
Matches 261; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY      1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGCAACATGCTAACGATGAGTTAGCAACA 60
DB      369 AATGTAGTCTTATGCAATACACTTGTAGTCTTGGCAACATGCTAACGATGAGTTAGCAACA 428
QY      61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
DB      429 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 488
QY      121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGGAATTGGAGCAAGCACTAAATT 180
DB      489 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGGAATTGGAGCAAGCACTAAATT 548
QY      181 CGCATTTGCAGAGAT-ATTGTATTATTAGTGCCTCGATACATAATAAACGCCAATTGAC 239
DB      549 CGCATTTGCAGAGATATTGTATTATTAGTGCCTCGATACATAATAAACGCCAATTGAC 608
QY      240 CATTCCACCACTTGGTGTGCACCTC 264
DB      609 CATTCCACCACTTGGTGTGCACCTC 633

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RESULT 17
US-09-897-006-9
; Sequence 9, Application US/09897006
; Patent No. US2002106729A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Expression Vectors
; FILE REFERENCE: GALA-06415
; CURRENT APPLICATION NUMBER: US/09/897,006
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 5130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-006-9
Query Match      87.9%; Score 232; DB 9; Length 5130;
Best Local Similarity 97.0%; Pred. No. 3.6e-69;
Matches 258; Conservative 0; Mismatches 5; Indels 3; Gaps 2;
QY      1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGCAACATGCTAACGATGAGTTAGCAACA 60
DB      2325 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGCAACATGCTAACGATGAGTTAGCAACA 2384
QY      61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
DB      2385 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 2444
QY      121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGGAATTGGAGCAAGCACTAAATT 180
DB      2445 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGGAATTGGAGCAAGCACTAAATT 2504
QY      181 CGCATTTGCAGAGAT-ATTGTATTATTAGTGCCTCGATACATAATAAACGCCA--TTTG 237
DB      2505 CGCATTTGCAGAGATATTGTATTATTAGTGCCTCGATACATAATAAACGCCA--TTTG 2564
QY      238 ACCATTCCACCACTTGGTGTGCACCT 263
DB      2565 ACCATTCCACCACTTGGTGTGCACCT 2590

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DB      2385 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 2444
QY      121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGGAATTGGAGCAAGCACTAAATT 180
DB      2445 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGGAATTGGAGCAAGCACTAAATT 2504
QY      181 CGCATTTGCAGAGAT-ATTGTATTATTAGTGCCTCGATACATAATAAACGCCA--TTTG 237
DB      2505 CGCATTTGCAGAGATATTGTATTATTAGTGCCTCGATACATAATAAACGCCA--TTTG 2564
QY      238 ACCATTCCACCACTTGGTGTGCACCT 263
DB      2565 ACCATTCCACCACTTGGTGTGCACCT 2590
RESULT 18
US-09-897-511A-9
; Sequence 9, Application US/09897511A
; Publication No. US20030092882A1
; GENERAL INFORMATION:
; APPLICANT: Brenel, Robert
; APPLICANT: Miller, Linda
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/09/897,511A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 5130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-511A-9
Query Match      87.9%; Score 232; DB 10; Length 5130;
Best Local Similarity 97.0%; Pred. No. 3.6e-69;
Matches 258; Conservative 0; Mismatches 5; Indels 3; Gaps 2;
QY      1 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGCAACATGCTAACGATGAGTTAGCAACA 60
DB      2325 AATGTAGTCTTATGCAATACCTTTGTAGTCTTGGCAACATGCTAACGATGAGTTAGCAACA 2384
QY      61 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 120
DB      2385 TGCCTTACAAGGAGAGAAAAAGCACCGTGCATGCCGATTGGTGGAAAGTAAGTGGTACGA 2444
QY      121 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGGAATTGGAGCAAGCACTAAATT 180
DB      2445 TCGTGCCTTATTAGGAGGCAACAGACGGGTCTGCATGGAATTGGAGCAAGCACTAAATT 2504
QY      181 CGCATTTGCAGAGAT-ATTGTATTATTAGTGCCTCGATACATAATAAACGCCA--TTTG 237
DB      2505 CGCATTTGCAGAGATATTGTATTATTAGTGCCTCGATACATAATAAACGCCA--TTTG 2564
QY      238 ACCATTCCACCACTTGGTGTGCACCT 263
DB      2565 ACCATTCCACCACTTGGTGTGCACCT 2590

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RESULT 19
US-10-155-736A-1
; Sequence 1, Application US/10155736A
; Publication No. US20030095948A1
; GENERAL INFORMATION:
; APPLICANT: Universit. di Torino
; TITLE OF INVENTION: Vector and methods of use for selective expression of genes in si
; TITLE OF INVENTION: of angiogenesis in vivo
; FILE REFERENCE: 36019/MNN

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; CURRENT APPLICATION NUMBER: US/10/155,736A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE:
; SEQ ID NO 1
; LENGTH: 10469
; TYPE: DNA
; ORGANISM: HIV-1
US-10-155-736A-1

Query Match      82.3%; Score 217.4; DB 14; Length 10469;
Best Local Similarity 99.1%; Pred. No. 5.6e-64;
Matches 229; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 60
DB 2218 MATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 2277
QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGGTGGAAAGTAAGTGGTACGA 120
DB 2278 TGCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGGTGGAAAGTAAGTGGTACGA 2337
QY 121 TCGTCCCTTATAGGAGGCAACAGAGCGGCTGTCATGATGATGGAGCAACCACTAAAT 180
DB 2338 TCGTCCCTTATAGGAGGCAACAGAGCGGCTGTCATGATGATGGAGCAACCACTAAAT 2397
QY 181 -CCGATTCGAGAGATATTGTATTAAAGTGCCTAGCTGATACATATAACG 230
DB 2398 GCGCATTCGAGAGATATTGTATTAAAGTGCCTAGCTGATACATATAACG 2448

RESULT 20
US-09-733-042-1
; Sequence 1, Application US/09733042
; Patent No. US20020168709A1
; GENERAL INFORMATION:
; APPLICANT: Hennecke, Frank
; APPLICANT: Renner, Wolfgang A.
; TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
; FILE REFERENCE: 1700.0100001
; CURRENT APPLICATION NUMBER: US/09/733,042
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/169,988
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 11282
; TYPE: DNA
; ORGANISM: pCpYts
US-09-733-042-1

Query Match      77.7%; Score 205.2; DB 9; Length 11282;
Best Local Similarity 98.6%; Pred. No. 9.6e-60;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 61
DB 664 ATCCAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 723
QY 62 GCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGGTGGAAAGTAAGTGGTACGAT 121
DB 724 GCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGGTGGAAAGTAAGTGGTACGAT 783
QY 122 CGTCCCTTATAGGAGGCAACAGAGCGGCTGTCATGATGATGCAACCACTAAATTC 181
DB 784 CGTCCCTTATAGGAGGCAACAGAGCGGCTGTCATGATGATGCAACCACTAAATTC 843
QY 182 CGCATTCGAGAGATATTGTATTAAAGTGCC 211
DB 844 CGCATTCGAGAGATATTGTATTAAAGTGCC 873

RESULT 21
US-09-275-883-1
; Sequence 1, Application US/09275883
; Publication No. US20030053988A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Wolfgang A.
; APPLICANT: Nieba, Lars
; APPLICANT: Boersma, Marco
; TITLE OF INVENTION: Inducible Alphaviral Gene Expression System
; FILE REFERENCE: 1700.0020001
; CURRENT APPLICATION NUMBER: US/09/275,883
; CURRENT FILING DATE: 1999-03-25
; EARLIER APPLICATION NUMBER: US 60/079,562
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cDNA
US-09-275-883-1

Query Match      77.7%; Score 205.2; DB 10; Length 11282;
Best Local Similarity 98.6%; Pred. No. 9.6e-60;
Matches 207; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATGTAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 61
DB 664 ATCCAGTCTTATGCAATACCTTGTAGTCTTGTGCAACATGTAACGATGAGTTAGCAACA 723
QY 62 GCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGGTGGAAAGTAAGTGGTACGAT 121
DB 724 GCCTTACAGGAGAGAAAAGCACCCTGTCATGCGGATGGTGGAAAGTAAGTGGTACGAT 783
QY 122 CGTCCCTTATAGGAGGCAACAGAGCGGCTGTCATGATGATGCAACCACTAAATTC 181
DB 784 CGTCCCTTATAGGAGGCAACAGAGCGGCTGTCATGATGATGCAACCACTAAATTC 843
QY 182 CGCATTCGAGAGATATTGTATTAAAGTGCC 211
DB 844 CGCATTCGAGAGATATTGTATTAAAGTGCC 873

RESULT 22
US-09-921-143-36
; Sequence 36, Application US/09921143
; Publication No. US20030215921A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Timothy
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112P6
; CURRENT APPLICATION NUMBER: US/09/921,143
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/223,276
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-921-143-36

Query Match      71.1%; Score 187.6; DB 11; Length 5283;
Best Local Similarity 91.5%; Pred. No. 8.2e-54;
Matches 214; Conservative 0; Mismatches 9; Indels 11; Gaps 1;

QY 41 GTRACGATGAGTTAGCAACATGCTTACAGAGAGAAAAGCACCCTGCGATGCCGATTCG 100

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; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid MMTV-E2a-SV40-Neo
US-09-847-101B-35

Query Match          65.7%; Score 173.4; DB 9; Length 11600;
Best Local Similarity 99.4%; Pred. No. 9.7e-49;
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTGAACGATGAGTTAGCAACA 60
      |||
Db 11426 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTGAACGATGAGTTAGCAACA 11485

QY 61 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAAGTGGTACGA 120
      |||
Db 11486 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAAGTGGTACGA 11545

QY 121 TCGTGCCCTTATTAGGAGCAACAGACGGGTCTGCATGATGGACGAAACCACT 175
      |||
Db 11546 TCGTGCCCTTATTAGGAGCAACAGACGGGTCTGCATGATGGACGAAACCACT 11600

RESULT 26
US-09-482-682-49
; Sequence 49, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482.682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-49

Query Match          65.7%; Score 173.4; DB 10; Length 11600;
Best Local Similarity 99.4%; Pred. No. 9.7e-49;
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTGAACGATGAGTTAGCAACA 60
      |||
Db 11426 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTGAACGATGAGTTAGCAACA 11485

QY 61 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAAGTGGTACGA 120
      |||
Db 11486 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAAGTGGTACGA 11545

QY 121 TCGTGCCCTTATTAGGAGCAACAGACGGGTCTGCATGATGGACGAAACCACT 175
      |||
Db 11546 TCGTGCCCTTATTAGGAGCAACAGACGGGTCTGCATGATGGACGAAACCACT 11600

RESULT 27
US-10-403-337-42
; Sequence 42, Application US/10403337
; Publication No. US20030215948A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Neo
US-10-403-337-42

Query Match          65.7%; Score 173.4; DB 15; Length 11600;
Best Local Similarity 99.4%; Pred. No. 9.7e-49;
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTGAACGATGAGTTAGCAACA 60
      |||
Db 11426 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGTGAACGATGAGTTAGCAACA 11485

QY 61 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAAGTGGTACGA 120
      |||
Db 11486 TGCCTTCAAGGAGAGAAAAGCCCGTGCATGCCGATGGTGAAGTAAAGTGGTACGA 11545

QY 121 TCGTGCCCTTATTAGGAGCAACAGACGGGTCTGCATGATGGACGAAACCACT 175
      |||
Db 11546 TCGTGCCCTTATTAGGAGCAACAGACGGGTCTGCATGATGGACGAAACCACT 11600

RESULT 28
US-10-351-890-42
; Sequence 42, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Neo
US-10-351-890-42

Query Match          65.7%; Score 173.4; DB 15; Length 11600;
Best Local Similarity 99.4%; Pred. No. 9.7e-49;
Matches 174; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTACGATGAGTTAGCAACA 60
Db 11426 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTACGATGAGTTAGCAACA 11485

QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGAGTAAGTGGTACGA 120
Db 11486 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGAGTAAGTGGTACGA 11545

QY 121 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGGAGCAACCACT 175
Db 11546 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGGAGCAACCACT 11600

RESULT 29
US-10-182-329-1
; Sequence 1, Application US/10182329
; Publication No. US20040005564A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAURO, Vincent P.
; APPLICANT: EDELMAN, Gerald M.
; APPLICANT: JONES, Frederick S.
; APPLICANT: OWENS, Geoffrey
; APPLICANT: MEECH, Robin
; TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRANSLATION
; FILE REFERENCE: SCRIPI380-1
; CURRENT APPLICATION NUMBER: US/10/182,329
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US 01/02733
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/261,312
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/230,956
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/230,852
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/207,804
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: US 60/186,496
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/178,815
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 6279
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: vector
US-10-182-329-1

Query Match 65.1%; Score 171.8; DB 15; Length 6279;
Best Local Similarity 98.9%; Pred. No. 2.6e-48;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 60
Db 203 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 262

QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGAGTAAGTGGTACGA 120
Db 263 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGAGTAAGTGGTACGA 322

QY 121 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGGAGCAACCACT 175
Db 323 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGGAGCAACCACT 377

RESULT 30
US-10-182-329-9
; Sequence 1, Application US/10182329
; Publication No. US20040005564A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAURO, Vincent P.
; APPLICANT: EDELMAN, Gerald M.
; APPLICANT: JONES, Frederick S.
; APPLICANT: OWENS, Geoffrey
; APPLICANT: MEECH, Robin
; TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRANSLATION
; FILE REFERENCE: SCRIPI380-1
; CURRENT APPLICATION NUMBER: US/10/182,329
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US 01/02733
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/261,312
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/230,956
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/230,852
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/207,804
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: US 60/186,496
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/178,815
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 6279
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: vector
US-10-182-329-1

Query Match 65.1%; Score 171.8; DB 15; Length 6279;
Best Local Similarity 98.9%; Pred. No. 2.6e-48;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 60
Db 203 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 262

QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGAGTAAGTGGTACGA 120
Db 263 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGAGTAAGTGGTACGA 322

QY 121 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGGAGCAACCACT 175
Db 323 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGGAGCAACCACT 377

RESULT 31
US-10-264-237-633
; Sequence 633, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 633

```

```

; Sequence 9, Application US/10182329
; Publication No. US20040005564A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: MAURO, Vincent P.
; APPLICANT: EDELMAN, Gerald M.
; APPLICANT: JONES, Frederick S.
; APPLICANT: OWENS, Geoffrey
; APPLICANT: MEECH, Robin
; TITLE OF INVENTION: METHODS OF IDENTIFYING SYNTHETIC TRANSCRIPTIONAL AND TRANSLATION
; FILE REFERENCE: SCRIPI380-1
; CURRENT APPLICATION NUMBER: US/10/182,329
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: PCT/US 01/02733
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/261,312
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/230,956
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/230,852
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/207,804
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: US 60/186,496
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/178,815
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 8513
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: vector
US-10-182-329-9

Query Match 65.1%; Score 171.8; DB 15; Length 8513;
Best Local Similarity 98.9%; Pred. No. 3e-48;
Matches 173; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 60
Db 203 AATGTAGTCTTATGCAATACCTCTTGTAGTCTTGCACATGGTAAAGTGGTACGA 262

QY 61 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGAGTAAGTGGTACGA 120
Db 263 TGCCTTACAGGAGAGAAAAGCACCCTGTCATCCGATTTGGAGTAAGTGGTACGA 322

QY 121 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGGAGCAACCACT 175
Db 323 TCGTCCCTTATTAGGAGGCAACAGACGGGTCTGCATGGATTTGGAGCAACCACT 377

RESULT 31
US-10-264-237-633
; Sequence 633, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 633

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/ LENGTH: 766
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (56)..(56)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (91)..(91)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (141)..(141)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (652)..(652)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (753)..(753)
/ OTHER INFORMATION: n equals a,t,g, or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (763)..(763)
/ OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-633

Query Match 61.1%; Score 161.2; DB 15; Length 766;
Best Local Similarity 89.8%; Pred. No. 4.4e-45;
Matches 199; Conservative 0; Mismatches 10; Indels 13; Gaps 2;

QY 55 GCACATGCTTCAAGGAGAGAAAAAGCACCGTCGATGCGATTGGTGAAGTAA-GGT 113
Db 9 GCACATGCTTATAGGAGAGAAAAAGCACCGTCGATGCGATTGGGAGTAGGGT 68

QY 114 GTATGATCGTG-----CATTAGGAAGCAACAGACGGTCTGCATGGA 161
Db 69 GTATGATCGTGATGATGTCGTCCTTTAGGAAGCAACAGACGGTCTGCATGGA 128

QY 162 TTGACCAACCACTAATTCGCGATTCAGAGATTTATTTAGTCTAGCTCGATA 221
Db 129 TTGACCAACCACTAATTCGCGATTCAGAGATTTATTTAGTCTAGCTCGATA 188

QY 222 CAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCACCT 263
Db 189 CAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCACCT 230

RESULT 32
US-10-267-117-5
; Sequence 5, Application US/10267117
; Publication No. US20030082162A1
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/10/267,117
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/299,141
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
US-10-267-117-5
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/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
US-10-267-117-5

Query Match 29.2%; Score 77; DB 14; Length 7492;
Best Local Similarity 98.9%; Pred. No. 1.7e-15;
Matches 88; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 177 AATTCGCATTGCAGAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATAAAGCCATT 235
Db 1 AATTCGCATTGCAGAGATTAATTGTATTTAAGTGGCTAGCTCGATACATAAAGCCATT 60

QY 236 TGACCATTCACACATTTGGTGTGCACCTC 264
Db 61 TGACCATTCACACATTTGGTGTGCACCTC 89

RESULT 33
US-10-340-112-5
; Sequence 5, Application US/10340112
; Publication No. US20030095949A1
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/10/340,112
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US/09/299,141
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-04-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
US-10-340-112-5

Query Match 29.2%; Score 77; DB 14; Length 7492;
Best Local Similarity 98.9%; Pred. No. 1.7e-15;
Matches 88; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 177 AATTCGCATTGCAGAGAT-ATTGTATTTAAGTGGCTAGCTCGATACATAAAGCCATT 235
Db 1 AATTCGCATTGCAGAGATTAATTGTATTTAAGTGGCTAGCTCGATACATAAAGCCATT 60

QY 236 TGACCATTCACACATTTGGTGTGCACCTC 264
Db 61 TGACCATTCACACATTTGGTGTGCACCTC 89

RESULT 34
US-10-192-085-10
; Sequence 10, Application US/10192085
; Publication No. US20020173030A1
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Parson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPHEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
```

```

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA: US/10/192,085
; APPLICATION NUMBER: US/10/192,085
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/389,394
; FILING DATE: 12-DEC-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
;
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-192-085-10

Query Match 19.6%; Score 51.8; DB 13; Length 74;
Best Local Similarity 96.4%; Pred. No. 9.7e-08;
Matches 53; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 176 AATTCGCGATTCCAGAGATATTGTTTAAAGTCGCTAGCTCGATACAATAACG 230
Db 1 AATTCGCGATTCCAGAGATATTGTTTAAAGTCGCTAGCTCGATACAATAACG 55

RESULT 35
US-10-192-085-11/c
; Sequence 11, Application US/10192085
; Publication No. US20020173030A1
;
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; Dulli, Thomas
; Parson, Deborah A.
; Witt, Rochelle
;
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/192,085
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365

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; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/389,394
; FILING DATE: 12-DEC-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
;
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-192-085-11

Query Match 18.9%; Score 50; DB 13; Length 74;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 CGCGATTCCAGAGATATTGTTTAAAGTCGCTAGCTCGATACAATAACG 230
Db 73 CGCGATTCCAGAGATATTGTTTAAAGTCGCTAGCTCGATACAATAACG 24

RESULT 36
US-09-725-720-9/c
; Sequence 9, Application US/09725720
; Patent No. US20010049136A1
;
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVITANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/725,720
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/379,452
; FILING DATE:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Radio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
;
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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QY 106 AGTAAGGTGGTACGATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGATTGG 165

Db 106 GGCAGTTAGGAGTATTGATTATGTTGGTAGGACAGACACTACTGCTTGGATTGG 165
QY 166 A 166
Db 166 A 166

RESULT 40

US-10-027-632-301875
; Sequence 301875, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 301875
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-301875

Query Match 12.5%; Score 33; DB 15; Length 542;
Best Local Similarity 54.5%; Pred. No. 0.8;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 46 GATGAGTTAGCAATGCTTACAGGAGAGAAAGCAACCGTCTCATGCGATTGGTGA 105
Db 46 GAGAAGTGACTGTCTGACTCACACTGGAATAGTAGAGACCGGTGGGACGAGGA 105
QY 106 AGTAAGTGTGACGATCGTGCCTTATTAGGAAGCAACAGCGGTCTGACATGGATTGG 165
Db 106 GGCAGTTAGGAGTATTGATTATGTTGGTAGGCAAGACACTACTGCTTGGATTGG 165
QY 166 A 166
Db 166 A 166

RESULT 41

US-10-027-632-50648
; Sequence 50648, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 50648
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-50648

Query Match 12.5%; Score 33; DB 15; Length 573;
Best Local Similarity 54.5%; Pred. No. 0.82;
Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 46 GATGAGTTAGCAATGCTTACAGGAGAGAAAGCAACCGTCTCATGCGATTGGTGA 105
Db 54 GAGAAGTGACTGTCTGACTCACACTGGAATAGTAGGAGACCGGTGGGACGAGGA 113
QY 106 AGTAAGTGTGACGATCGTGCCTTATTAGGAAGCAACAGCGGTCTGACATGGATTGG 165
Db 114 GGCAGTTAGGAGTATTGATTATGTTGGTAGGCAAGACACTACTGCTTGGATTGG 173
QY 166 A 166
Db 174 A 174

RESULT 42

US-10-369-493-25133/c
; Sequence 25133, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10/52052/B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 25133
; LENGTH: 2877
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-25133

Query Match 12.2%; Score 32.2; DB 15; Length 2877;
Best Local Similarity 51.0%; Pred. No. 3.4;
Matches 76; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 88 TGCATGCCGATGGTGAAGTGGTGTAGGATCGTGCCTTATTAGGAAGCAACAGAC 147
Db 2193 TGGATTCCGATTGAAGATGTGACGTAGTCCCTTTGTTAGCAGGTATGGAACCTTC 2134
QY 148 GGGTCTGATGGATTGGACGAACCACTAAATTCGCCATTGCAGAGATATGTATTAAAG 207
Db 2133 GAGTCTGCAATGTGACATCCAGGCCATATTTCATCAAAATTTCAATATATCCATGTTTG 2074
QY 208 TGCCTAGCTCGATACAAATAAAGCCCATTT 236

```
Db      2073 AGTGTAGTTAGACACTACGACGACCTTCT 2045

RESULT 43
US-10-424-599-52313/c
; Sequence 52313, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 52313
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_18252C.1
US-10-424-599-52313

Query Match      11.9%; Score 31.4; DB 12; Length 669;
Best Local Similarity 54.9%; Pred. No. 3.2; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY      116 TAGCATGTGCTTATTAGGAAGCAACAGACGGTCTGACATGGATGGACGAGCAACT 175
Db      531 TTCCATCGGCCCGCTATAGGGTGGCTACCACTAATAATACATAGATGCATTAACCCACC 472

QY      176 AATTCGCCATTCGACAGATATCTATTAGTGGCTAGCTCGATACATATAA 228
Db      471 CGATGGGCAATGAATCTCATCAAGTATCTAGCAGGTAGGAGTATATAATATA 419

RESULT 44
US-10-424-599-132712/c
; Sequence 132712, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 132712
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90846C.1
US-10-424-599-132712

Query Match      11.7%; Score 31; DB 12; Length 595;
Best Local Similarity 52.8%; Pred. No. 4.1; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY      17 ATACTCTTAGTCTTGGCAACATGTTAACGATGATAGCAACATGCTTACCAAGGAG 76
Db      133 AGACTGTGTTAATTTGGTGAATAATGGTTTGGATAAAGCAACACGGTCTTTGAGGGTGATAG 74

QY      77 AAAAGACCGCTCGATCGGATTCGGTGAAGTAAAGTGTACGATCGTCCCTTATTAGGA 136
Db      73 AGCATGCACCAAGCTTGTTAATGATAAGACTAATGTGATGAGTGTGTGTATGAGGA 14

RESULT 45
US-10-424-599-14875
; Sequence 14875, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 14875
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_113438C.1
US-10-424-599-14875

Query Match      11.7%; Score 30.8; DB 12; Length 1330;
Best Local Similarity 51.4%; Pred. No. 7.1; Indels 0; Gaps 0;
Matches 71; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY      5 TAGCTTTATGCAATCTCTTGTAGTCTTTGCAACATGCTGAACGATGATGAGTTAGCAATGCC 64
Db      1038 TAGCATTATTATCATGATTTTCTGTAGGAAATGAAGGGAACCAAGCAAGCAAAATATA 1097

QY      65 TTACAGAGAGAGAAAAGCAACCGTGCATGCCGATTGGTGGAGTAAGGTGGTACGATCGT 124
Db      1098 TTTTAGACTGGAAAAGCAATCATAGATGCGAAGCGCGGCAAAACAAAGGATATGAAGT 1157

QY      125 GCCTTATTAGGAAGCA 142
Db      1158 GGCATTAAAGAAATGGAA 1175

RESULT 46
US-10-027-632-112120/c
; Sequence 112120, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
```

; SEQ ID NO 112120
; LENGTH: 2664
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-112120

Query Match 11.7%; Score 30.8; DB 15; Length 2664;
Best Local Similarity 61.0%; Pred. No. 9.9;
Matches 50; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 10 TTATGCAATATCTTGTAGTCTTGCACATGGTAACGATGAGTAGCAACATGCCCTTACA 69
Db 600 TTATGTAATACACTTATAGATATGTCACACTGTAACTCATATTAATTACATCACCTTAAA 541
QY 70 AGGAGAGAAAAAGCACCGTGCA 91
Db 540 GGAATATAAAGCAGCAGTGCA 519

RESULT 47

US-10-027-632-175173
; Sequence 175173, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175173
; LENGTH: 5214
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-175173

Query Match 11.6%; Score 30.6; DB 15; Length 5214;
Best Local Similarity 50.3%; Pred. No. 16;
Matches 75; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 8 TCTTATGCATATCTTGTAGTCTTGCACATGGTAACGATGAGTAGCAACATGCCCTTA 67
Db 3021 TATAAGGTATTTCTTTTAAAGAAAGAAATGGCAATCTGACTTAGAAAAATCGGCTC 3080
QY 68 CAAGGAGAGAAAAAGCACCGTGCGATTCGGTGAAGTAAGTGAGTACGATCGTCC 127
Db 3081 AAAGGAATCTAGAGACACCGCATCCATAGGTGATGCTGATGATGATGATGCT 3140
QY 128 TTATTAGGAAGCAACAGACGGGTCTGAC 156
Db 3141 AAGTTAGCAATCTATCATCATGGGGCTCTCAC 3169

RESULT 48

US-10-425-114-31887
; Sequence 31887, Application US/10425114
; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31887
; LENGTH: 3300
; TYPE: DNA
; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMFLB73227A02_FLI
US-10-425-114-31887

Query Match 11.5%; Score 30.4; DB 12; Length 3300;
Best Local Similarity 50.7%; Pred. No. 15;
Matches 73; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 110 AGGTGTACATCTGCTTATTAGGAAGGCAACAGACGGGTCTGCATGATTGGACGA 169
Db 2354 AGTCCAGCAACTTGACATGGAGAGCCCAATCAAAAGGAGCTTGAAGAATGGATAT 2413
QY 170 ACCATTAATTCGCATTCGAGAGATATTTATTAAAGTGCTAGCTCGATACAATPAAC 229
Db 2414 ACCAATGAAGTTGTGTTGAATAGAGTGCTTGGAAAGAAAGCTACCCACGTGCCGACC 2473
QY 230 GCCATTGACCATTCACCATTTG 253
Db 2474 GTGATTGAGCATTTTTCCTTATAG 2497

RESULT 49

US-09-739-254-63
; Sequence 63, Application US/09739254
; Patent No. US20010021700A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: PZ032P1
; CURRENT APPLICATION NUMBER: US/09/739,254
; CURRENT FILING DATE: 2000-12-19
; EARLIER APPLICATION NUMBER: 09/511,554
; EARLIER FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: PCT/US99/19330
; EARLIER FILING DATE: 1999-08-24
; EARLIER APPLICATION NUMBER: 60/097,917
; EARLIER FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 60/098,634
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: SITE
; LOCATION: (282)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (607)

RESULT 51
US-10-054-988-63
US; Sequence 63, Application US/10054988

```

: SEQ ID NO 63
: LENGTH: 1202
: TYPE: DNA
: ORGANISM: Homo sapiens

```


Query Match	11.4%	Score 30.2;	DB 9;	Length 1452;
Best Local Similarity	53.4%;	Pred. No. 12;		
Matches 62;	Conservative 0;	Mismatches 54;	Indels 0;	Gaps 0;
Qy	17	ATACTCTTGAGTCTTGCACATGGTAACGATGAGTTAGCAATGCCTTACAGAGAG	76	
Db	485	ACACCCAGGTGGTGAAGTCTTAAGGATAAGTGGAAATTTGCCCATAGCTGTCTCTGCACAG	544	
Qy	77	AAAAAGACCGTGCATGCCGATTGGTGGAGTAGGTGATAGTCGTGGCCTTAAT	132	
Db	545	AAACTGTCCCGAGAGAGAATGAATGGAGGACATAGGGCTCTGGTGCCCAACNTTTT	600	

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RESULT 54
US-09-904-615-34
; Sequence 34, Application US/09904615
; Patent No. US20020026040A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0

```

```

1 PRIOR FILING DATE: 1998-08-25
2
3 PRIOR APPLICATION NUMBER: 60/098,634
4
5 PRIOR FILING DATE: 1998-08-31
6
7 NUMBER OF SEQ ID NOS: 170
8
9 SOFTWARE: PatentIn Ver. 2.0
10
11 SEQ ID NO 34
12
13 LENGTH: 1452
14
15 TYPE: DNA
16
17 ORGANISM: Homo sapiens
18
19 FEATURE:
20
21 NAME/KEY: SITE
22
23 LOCATION: (283)
24
25 OTHER INFORMATION: n equals a,t,g, or c
26
27 NAME/KEY: SITE
28
29 LOCATION: (596)
30
31 OTHER INFORMATION: n equals a,t,g, or c
32
33 NAME/KEY: SITE
34
35 LOCATION: (607)
36
37 OTHER INFORMATION: n equals a,t,g, or c
38
39 NAME/KEY: SITE
40
41 LOCATION: (1275)
42
43 OTHER INFORMATION: n equals a,t,g, or c
44
45 NAME/KEY: SITE
46
47 LOCATION: (1284)
48
49 OTHER INFORMATION: n equals a,t,g, or c
50
51 US-09-904-615-34

```

Query Match	11.4%	Score 30.2;	DB 9;	Length 1452;
Best Local Similarity	53.4%;	Pred. No. 12;		
Matches	62;	Conservative 0;	Mismatches 54;	Indels 0;
Gaps	0;			
QY	17	ATACTCTTTGAGTCTTGCACATGTTACGATGAGTTACAAATGCTTACAGAGAG	76	
Db	485	ACACCAGGTGGTGAGTCTTAAAGATAAGTGGAAATTTGCCCCATAGCTCTCTCGACAG	544	
QY	77	AAAGAAGACCGTGATGCCGATTTGTGGAGTAAAGTGTGATCTGCGCTTATT	132	
Db	545	AAACTGTCCACGAAGAATCAATGAGACATAGGGCTGTGGTCCCACTTTT	600	

RESULT 55.
US-10-054-988-34
; Sequence 34, Application US/10054988
; Publication No. US20030087341A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

```
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/10/054,988
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/904,615
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-054-988-34

Query Match
Best Local Similarity 11.4%; Score 30.2; DB 14; Length 1452;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 17 ATACTCTTGTAGTCTTGCACATGTAAGCATGTAAGTGTAGCAATGCTTACAGGAGGAG 76
Db 485 ACACCCAGGTGTGAGTCTTAAAGATAAGGTGAATTTGCCCATAGCTGTCTGGACAG 544

QY 77 AAAAGCACCGTCGATGCGGATGCTGGAGTAAAGTGTAGCATCGTGCCTTATT 132
Db 545 AAATGCCAGAGAGATGAATGAGGACATAGGGCTCTGTGTGCCACCCNTTTT 600

RESULT 56
US-10-055-098-34
; Sequence 34, Application US/10055098
; Publication No. US2003013954A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/10/055,098
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/19330
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (283)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (607)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1284)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-055-098-34

Query Match
Best Local Similarity 11.4%; Score 30.2; DB 14; Length 1452;
Matches 62; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 17 ATACTCTTGTAGTCTTGCACATGTAAGCATGTAAGTGTAGCAATGCTTACAGGAGGAG 76
Db 485 ACACCCAGGTGTGAGTCTTAAAGATAAGGTGAATTTGCCCATAGCTGTCTGGACAG 544

QY 77 AAAAGCACCGTCGATGCGGATGCTGGAGTAAAGTGTAGCATCGTGCCTTATT 132
Db 545 AAATGCCAGAGAGATGAATGAGGACATAGGGCTCTGTGTGCCACCCNTTTT 600

RESULT 57
US-10-027-632-165752/c
; Sequence 165752, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165752
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-165752

Query Match
Best Local Similarity 11.4%; Score 30; DB 15; Length 834;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 153 TGACATGATTTGGACGACCACTAAATTCGCGATTCGACGATATTTTAAAGTGCCT 212
Db 325 TGAACATATCTTTTGTATCCACCTGCTATCTTTTGGCAATTTATATATATAGCCT 266

QY 213 AGTCGATATCAATAAACGCCATTTGACCATTCACCAATGG 254
```

```
Db 265 AGCTCTAAGGATTAAAGTATTTCAGTTTTCACCACTCTGG 224
|||||
Query Match 11.4%; Score 30; DB 15; Length 834;
Best Local Similarity 55.9%; Pred. No. 11;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

RESULT 58
US-10-027-632-165753/c
; Sequence 165753, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 165753
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-165753

Query Match 11.4%; Score 30; DB 15; Length 834;
Best Local Similarity 55.9%; Pred. No. 11;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 153 TGACATGATTGGACGACCACTAAATTCGCGATTGCAGAGATATTGTTTAAGTGCCT 212
Db 325 TGAATATCTTTTGGTATCCATCGTATCTTTTTTTGGCAATTTTATTATTAAAGCCT 266
QY 213 AGCTGATACAAATAAAGCCATTGGACCATTCACCACTGG 254
Db 265 AGCTCTAAGGATTAAAGTATTTCAGTTTTCACCACTCTGG 224

RESULT 59
US-10-398-221-1044
; Sequence 1044, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1044
; LENGTH: 2271
; TYPE: DNA
; ORGANISM: Listeria monocytogenes-EGD
US-10-398-221-1044
```

```
Query Match 11.2%; Score 29.6; DB 15; Length 2271;
Best Local Similarity 68.3%; Pred. No. 24;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 25 GTAGTCTTGCAACATGTAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAAAGCA 84
Db 2020 GAAGTCGTGCACTTTATATTCATGATATGGAAGCAAGCATTACTTAGAAGAAAAAGAA 2079

RESULT 60
US-10-398-221-2861
; Sequence 2861, Application US/10398221.
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2861
; LENGTH: 2271
; TYPE: DNA
; ORGANISM: Listeria monocytogenes EGD
US-10-398-221-2861

Query Match 11.2%; Score 29.6; DB 15; Length 2271;
Best Local Similarity 68.3%; Pred. No. 24;
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 25 GTAGTCTTGCAACATGTAACGATGAGTTAGCAACATGCTTTACAAGGAGAGAAAAAGCA 84
Db 2020 GAAGTCGTGCACTTTATATTCATGATATGGAAGCAAGCATTACTTAGAAGAAAAAGAA 2079

RESULT 61
US-09-962-832-154
; Sequence 154, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 154
; LENGTH: 302250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-154

Query Match 11.2%; Score 29.6; DB 9; Length 302250;
Best Local Similarity 56.0%; Pred. No. 2.4e+02;
Matches 56; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 158 TGGATTGGACGAACCACTAAATTCGCGATTGCAGAGATATTGTTTAAGTGCCTAGCTC 217
Db 95902 TGTATAGAGGTACTAGCCAGTGCAGTAAATGCTAAGCAGATGAATCAAGGGCTAGAGA 95961
QY 218 GATACATAAACGCCATTGACCAATTCACCAATTTGGTGT 257
```

Db 95962 TAAAAATAAACAAATTTGGCTAATTACAGATGCTTTT 96001

RESULT 62

US-10-027-632-63861/c
; Sequence 63861, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63861
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-63861

Query Match 11.1%; Score 29.2; DB 15; Length 183;
Best Local Similarity 50.7%; Pred. No. 9.8;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 113 TGGTACGATCGCTGCTTATTAGGAGGCAACAGACGGGTCTGCATCGATTGGACGAACC 172
Db 145 TGGAGGTACATGAGTGTCTCTGAGGCAGTGCAGGGGAATAAGTATTTCATGGACGGAGT 86
QY 173 ACTAAATTCGGCATTCGACAGATATTGTTAAAGTGCCTAGCTCGATACATAAAGCC 232
Db 85 ACTGGTTCTTAAATTTTACAATTTGTTAAGTACTCTCTTAATCCAGTCTGTAC 26
QY 233 ATTGACCATTCACACA 250
Db 25 ATTCTAGAACTGAGRCA 8

RESULT 63

US-10-027-632-64765/c
; Sequence 64765, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64765
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-64765

Query Match 11.1%; Score 29.2; DB 15; Length 637;
Best Local Similarity 50.7%; Pred. No. 18;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 113 TGGTACGATCGCTGCTTATTAGGAGGCAACAGACGGGTCTGCATCGATTGGACGAACC 172
Db 599 TGGAGGTACATGAGTGTCTCTGAGGCAGTGCAGGGGAATAAGTATTTCATGGACGGAGT 540
QY 173 ACTAAATTCGGCATTCGACAGATATTGTTAAAGTGCCTAGCTCGATACATAAAGCC 232
Db 539 ACTGGTTCTTAAATTTTACAATTTGTTAAGTACTCTCTTAATCCAGTCTGTAC 480
QY 233 ATTGACCATTCACACA 250
Db 479 ATTCTAGAACTGAGRCA 462

RESULT 64

US-10-027-632-63862/c
; Sequence 63862, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63862
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-63862

Query Match 11.1%; Score 29.2; DB 15; Length 752;
Best Local Similarity 50.7%; Pred. No. 19;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 113 TGGTACGATCGCTGCTTATTAGGAGGCAACAGACGGGTCTGCATCGATTGGACGAACC 172
Db 714 TGGAGGTACATGAGTGTCTCTGAGGCAGTGCAGGGGAATAAGTATTTCATGGACGGAGT 655
QY 173 ACTAAATTCGGCATTCGACAGATATTGTTAAAGTGCCTAGCTCGATACATAAAGCC 232

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Db 654 ACTGTTCTAAATTTTACAAATGTTATGTTTAAAGTGAATCTCTTAATCCAGTGTCTGTAC 595
QY 233 ATTTCACCAATTCACCA 250
Db 594 ATTCTAGAAGTGAAGCA 577

```

```

RESULT 65
US-10-027-632-64766/c
; Sequence 64766, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64766
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-64766

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```

Query Match 11.1%; Score 29.2; DB 15; Length 752;
Best Local Similarity 50.7%; Pred. No. 19;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 113 TGGTAGCATCTGCTTATTAGGAAGGCAACAGACGGGTCTGCATCGATTCGACGAACC 172
Db 714 TCGAAGGTACATGAGTCTTCTGAGGCGAGTGAAGGGAATAGTATTTCATGGACGGAGT 655
QY 173 ACTAAATTCGCAATTCGAGATATTGTTTAAAGTCTAGCTCGATACATAAAACGCC 232
Db 654 ACTGTTTCTAAATTTTACAAATGTTATGTTTAAAGTGAATCTCTTAATCCAGTGTCTGTAC 595
QY 233 ATTTCACCAATTCACCA 250
Db 594 ATTCTAGAAGTGAAGCA 577

```

```

RESULT 66
US-10-027-632-310455/c
; Sequence 310455, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

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; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310455
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-310455

Query Match 11.1%; Score 29.2; DB 15; Length 752;
Best Local Similarity 50.7%; Pred. No. 19;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 113 TGGTAGCATCTGCTTATTAGGAAGGCAACAGACGGGTCTGCATCGATTCGACGAACC 172
Db 714 TCGAAGGTACATGAGTCTTCTGAGGCGAGTGAAGGGAATAGTATTTCATGGACGGAGT 655
QY 173 ACTAAATTCGCAATTCGAGATATTGTTTAAAGTCTAGCTCGATACATAAAACGCC 232
Db 654 ACTGTTTCTAAATTTTACAAATGTTATGTTTAAAGTGAATCTCTTAATCCAGTGTCTGTAC 595
QY 233 ATTTCACCAATTCACCA 250
Db 594 ATTCTAGAAGTGAAGCA 577

```

```

RESULT 67
US-10-027-632-310456/c
; Sequence 310456, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 310456
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-310456

```

```

Query Match 11.1%; Score 29.2; DB 15; Length 752;
Best Local Similarity 50.7%; Pred. No. 19;
Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 113 TGGTAGCATCTGCTTATTAGGAAGGCAACAGACGGGTCTGCATCGATTCGACGAACC 172

```

Db 714 TGAAGGTACATGAGTTCCTGAGCGAGTACAGAGGAATAAGTATTCATGGGACGGAGT 655
 QY 173 ACTAAATTCGCGATTCGACAGATATGTTTAAAGTGCTAGCTCGATACATTAACGCC 232
 Db 654 ACTGGTTCCTAAATTTACAAATGTTATGTTTAAAGTACTCTCTTAATCCAGTGTGTAC 595
 QY 233 ATTGACCATTCACCA 250
 Db 594 ATTCTAGAACTGAGGCA 577

RESULT 68

US-10-027-632-35424/c
 ; Sequence 35424, Application US/10027632
 ; Publication No. US20030204075A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
 ; TITLE OF INVENTION: Polymorphisms in the Human Genome
 ; FILE REFERENCE: 10827.129

; CURRENT APPLICATION NUMBER: US/10/027,632
 ; PRIOR FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 35424
 ; LENGTH: 766
 ; TYPE: DNA
 ; ORGANISM: Human
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

US-10-027-632-35424

Query Match 11.1%; Score 29.2; DB 15; Length 766;
 Best Local Similarity 50.7%; Pred. No. 19;
 Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 113 TGGTACGTCGCGCTTATTAGGAGGCAACAGAGCGGTCTGACATGGATTGGACGACC 172
 Db 714 TGGAGGTACATGAGTGTCTGAGGAGTGGAGGAATAAGTATTCATGGGACGGAGT 655
 QY 173 ACTAAATTCGCGATTCGACAGATATGTTTAAAGTGCTAGCTCGATACATTAACGCC 232
 Db 654 ACTGGTTCCTAAATTTACAAATGTTATGTTTAAAGTACTCTCTTAATCCAGTGTGTAC 595
 QY 233 ATTGACCATTCACCA 250
 Db 594 ATTCTAGAACTGAGGCA 577

RESULT 69

US-10-311-455-820
 ; Sequence 820, Application US/10311455
 ; Publication No. US20030143606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OLEK, Alexander
 ; APPLICANT: PIEPENBROCK, Christian
 ; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
 ; TITLE OF INVENTION: cytosine methylation
 ; FILE REFERENCE: 5013.1014

; CURRENT APPLICATION NUMBER: US/10/311,455
 ; CURRENT FILING DATE: 2002-12-16
 ; PRIOR APPLICATION NUMBER: PCT/EP01/07537
 ; PRIOR FILING DATE: 2001-07-02
 ; PRIOR APPLICATION NUMBER: DE 10032529.7
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: DE 10043826.1
 ; PRIOR FILING DATE: 2000-09-01
 ; NUMBER OF SEQ ID NOS: 2424
 ; SEQ ID NO 820
 ; LENGTH: 5297
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-311-455-820

Query Match 11.1%; Score 29.2; DB 14; Length 5297;
 Best Local Similarity 50.7%; Pred. No. 49;
 Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
 QY 70 AGGAGAGAAAAGCACCGTGCATGCCATTTGGTGAAGTAAGTGTGACATCGTCCTT 129
 Db 2592 AAGAAAGGAGAGAGTATAAATTTATGATAGTGAATTTATAATGTTGTTTTTTT 2651
 QY 130 ATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGAGCAACCACTAAATCCGCATTGC 189
 Db 2652 TTTAGAAGTAAGTAAGGTAGTATAAATTTATTGAGGTATAGATTAAATTTATTGA 2711
 QY 190 AGAGATATTGTTTAAAG 207
 Db 2712 GTATTATTATTATGTTAG 2729

RESULT 70

US-10-257-166-84
 ; Sequence 84, Application US/10257166
 ; Publication No. US2004002320A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OLEK, Alexander
 ; APPLICANT: PIEPENBROCK, Christian
 ; APPLICANT: BERLIN, Kurt
 ; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
 ; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
 ; FILE REFERENCE: 5013.1011
 ; CURRENT APPLICATION NUMBER: US/10/257,166
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: PCT/EP01/07470
 ; DE 10032529.7
 ; DE 10043826.1
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR FILING DATE: 2000-06-30
 ; 2000-09-01
 ; NUMBER OF SEQ ID NOS: 178
 ; SEQ ID NO 84
 ; LENGTH: 5297
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-257-166-84

Query Match 11.1%; Score 29.2; DB 16; Length 5297;
 Best Local Similarity 50.7%; Pred. No. 49;
 Matches 70; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
 QY 70 AGGAGAGAAAAGCACCGTGCATGCCATTTGGTGAAGTAAGTGTGACATCGTCCTT 129
 Db 2592 AAGAAAGGAGAGTATAAATTTATGATAGTGAATTTATAATGTTGTTTTTTT 2651
 QY 130 ATTAGGAAGGCAACAGACGGGTCTGACATGGATTGGAGCAACCACTAAATCCGCATTGC 189
 Db 2652 TTTAGAAGTAAGTAAGGTAGTATAAATTTATTGAGGTATAGATTAAATTTATTGA 2711

	Query Match	11.0%	Score 29	DB 9	Length 1438	
	Best Local Similarity	57.0%	Pred. No. 31			
	Matches 53	Conservative 0	Mismatches 40	Indels 0	Gaps 0	
Qy	23	TTGTAGTCTTGCAACATGTTAAGCATGAGTTAGCAACATGCTTACAGGAGAGAAAG	82			
Db	1382	TGCTGAACCTTACAANAATAGTACGACGAGTGAAGAAAGACTTCATAACGAGGAAAAGAC	1323			
Qy	83	CACCGTGATGCCGATTTGTTGAAGTAAAGTTG	115			
Db	1322	CAACCGGAGACCACGGCGGCCACCCAGGAGG	1290			

RESULT 75
US-10-097-534-5

```
; Sequence 5, Application US/10097534
; Publication No. US20030049607A1
; GENERAL INFORMATION:
; APPLICANT: GREENER, TSVIKA
; APPLICANT: MOSKOWITZ, HAIM
; APPLICANT: REISS, YUVAL
; APPLICANT: ALROY, IRIS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF VIRAL
; TITLE OF INVENTION: MATURATION
; FILE REFERENCE: PLV-001.01
; CURRENT APPLICATION NUMBER: US/10/097,534
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,224
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/308,958
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/340,170
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-534-5
```

```
Query Match      11.0%; Score 29; DB 14; Length 6102;
Best Local Similarity 55.4%; Pred. No. 61;
Matches 56; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY      16 AATACTCTGTAGTCTTGCACATGGTACGATGAGTTAGCACATGCGCTTACAGGAGA 75
Db      3248 AACATTTTGAATGCTGACAGCGCTCAGCCACGCTTAGCAAGAACCCACACACTCAGG 3307

QY      76 GAAAAAGCACCGTCGATGCCGATTTGGTGGAGCTAAGGTGGT 116
Db      3308 GAGAAATCCATTACATTGCGACTGAGGGTATCACGGGCT 3348
```

Search completed: March 11, 2004, 11:20:22
Job time : 194.633 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 05:54:28 ; Search time 352.355 Seconds
(without alignments)
7749.596 Million cell updates/sec

Title: US-09-733-368a-1_COPY_550_612

Perfect score: 63

Sequence: 1 tttaagtgcgtacgcgata.....accacattggtgcacctc 63

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hrg.*
- 3: gb_in.*
- 4: gb_em.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	63	100.0	101	6	B51991	E51991 Promoter, r
2	63	100.0	648	6	AX175190	AX175190 Sequence
3	63	100.0	648	6	AX175195	AX175195 Sequence
4	63	100.0	2309	12	EVU67090	U67090 Expression
5	63	100.0	2794	12	EVU51722	U51722 Expression
6	63	100.0	2856	12	AY229985	AY229985 Expressio
7	63	100.0	2895	12	AY229986	AY229986 Expressio
8	63	100.0	2981	12	EVU51721	U51721 Expression
9	63	100.0	3059	12	EVU67091	U67091 Expression
10	63	100.0	3189	6	A30504	A30504 plasmid p79
11	63	100.0	3277	6	A30505	A30505 plasmid p23
12	63	100.0	3277	6	A30507	A30507 plasmid p79
13	63	100.0	3384	6	A30503	A30503 plasmid p26
14	63	100.0	3427	6	A30513	A30513 plasmid p26
15	63	100.0	3427	6	A30515	A30515 plasmid p26
16	63	100.0	3557	12	SYNRSV3MV	M83240 Cloning vec
17	63	100.0	3979	6	A30511	A30511 plasmid p26
18	63	100.0	3980	6	A30509	A30509 plasmid p26
19	63	100.0	4059	6	AR071324	AR071324 Sequence
20	63	100.0	4341	6	A38214	A38214 Sequence 58
21	63	100.0	4341	6	AX286570	AX286570 Sequence
22	63	100.0	4457	6	AX743954	AX743954 Sequence
23	63	100.0	4839	12	SYNRSV5GFT	M83236 Cloning vec
24	63	100.0	5108	12	SYNRSV5NEO	M83237 cDNA expres
25	63	100.0	5564	12	SYNTCRC	I36555 Cloning vec
26	63	100.0	5653	6	I56772	I56772 Sequence 3
27	63	100.0	5653	6	I95540	I95540 Sequence 1
28	63	100.0	5736	12	SYNRSVNEO	M7786 prsVNeo clo
29	63	100.0	6836	6	AR215114	AR215114 Sequence
30	63	100.0	6836	6	AR302356	AR302356 Sequence
31	63	100.0	6836	6	AR373228	AR373228 Sequence
32	63	100.0	6836	6	AR401614	AR401614 Sequence
33	63	100.0	6836	12	AP346624	AP346624 PAGE vect
34	63	100.0	6864	12	XXU19931	U19931 Cloning vec
35	63	100.0	6926	6	A48775	A48775 Sequence 2
36	63	100.0	6926	6	AR018703	AR018703 Sequence
37	63	100.0	7086	6	AX743955	AX743955 Sequence
38	63	100.0	7334	6	AX743956	AX743956 Sequence
39	63	100.0	7492	6	AR235458	AR235458 Sequence
40	63	100.0	8238	6	BD268239	BD268239 Adenoviru
41	63	100.0	8413	12	XXU02432	U02432 Cloning vec
42	63	100.0	8475	12	XXU02430	U02430 Cloning vec
43	63	100.0	8591	6	I58322	I58322 Sequence 6
44	63	100.0	8591	6	I58323	I58323 Sequence 8
45	63	100.0	8591	6	I60508	I60508 Sequence 6
46	63	100.0	8591	6	I60509	I60509 Sequence 6
47	63	100.0	8591	6	I77052	I77052 Sequence 8
48	63	100.0	8591	6	I77053	I77053 Sequence 6
49	63	100.0	8591	6	I87173	I87173 Sequence 8
50	63	100.0	8591	6	I87174	I87174 Sequence 8
51	63	100.0	9184	12	XXU02431	U02431 Cloning vec
52	63	100.0	9737	6	AR215118	AR215118 Sequence
53	63	100.0	9737	6	AR215119	AR215119 Sequence
54	63	100.0	9737	6	AR215124	AR215124 Sequence
55	63	100.0	9737	6	AR302360	AR302360 Sequence
56	63	100.0	9737	6	AR302361	AR302361 Sequence
57	63	100.0	9737	6	AR302366	AR302366 Sequence
58	63	100.0	9737	6	AR373232	AR373232 Sequence
59	63	100.0	9737	6	AR373233	AR373233 Sequence
60	63	100.0	9737	6	AR373238	AR373238 Sequence
61	63	100.0	9737	6	AR401618	AR401618 Sequence
62	63	100.0	9737	6	AR401619	AR401619 Sequence
63	63	100.0	9737	6	AR401624	AR401624 Sequence
64	63	100.0	9871	6	AR215120	AR215120 Sequence
65	63	100.0	9871	6	AR302362	AR302362 Sequence

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66 63 100.0 9871 6 AR373234 Sequence
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68 63 100.0 10060 6 AR215121 Sequence
69 63 100.0 10060 6 AR302363 Sequence
70 63 100.0 10060 6 AR373235 Sequence
71 63 100.0 10060 6 AR401621 Sequence
72 63 100.0 10339 12 U02448 Cloning vec
73 63 100.0 10737 12 XXU02428 Cloning vec
74 63 100.0 10850 12 U02455 Cloning vec
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76 63 100.0 11265 6 BD084805 Enhanceme
77 63 100.0 11658 6 BD268238 Adenoviru
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79 63 100.0 37808 6 AX001082 Sequence
80 62 98.4 170 14 ALVLR3JB
81 62 98.4 190 14 RERSV5
82 62 98.4 231 5 CHRALV2
83 62 98.4 237 14 RERAV2
84 62 98.4 243 14 ALVLR3JA
85 62 98.4 249 14 RERSV4
86 62 98.4 306 14 GCERB
87 62 98.4 315 14 REASV1
88 62 98.4 330 14 ALRSV4OLTR
89 62 98.4 341 14 RERSV2
90 62 98.4 346 14 ALELTR2
91 62 98.4 346 14 RERSV3
92 62 98.4 348 14 ALVHLTCU
93 62 98.4 348 14 RERAV1
94 62 98.4 377 14 ALVLR3L1
95 62 98.4 387 14 ALVLR3L2
96 62 98.4 400 14 ALVLR3L4
97 62 98.4 565 6 AR202606 Sequence
98 62 98.4 565 6 BD005483 Cellular
99 62 98.4 565 14 U41728
100 62 98.4 633 14 ALRPROLTB

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ALIGNMENTS

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RESULT 1
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LOCUS 101 bp DNA linear PAT 31-JAN-2002
DEFINITION Promoter, recombinant containing the same and utilization thereof.
ACCESSION E51991
VERSION E51991.1 GI:18629552
KEYWORDS JP 2001000188-A/6.
SOURCE Rous sarcoma virus
ORGANISM Rous sarcoma virus
REFERENCE 1 (bases 1 to 101)
AUTHORS Kubomura,M. and Saito,S.
TITLE Promoter, recombinant containing the same and utilization thereof
JOURNAL Patent: JP 2001000188-A 6 09-JAN-2001;
NIPPON ZEON CORP
COMMENT OS Rous sarcoma virus
PN JP 2001000188-A/6
PD 09-JAN-2001
PF 22-JUN-1999 JP 1999174604
PR MAYUMI KUBOMURA, SHUJI SAITO
PC C12N15/09,A61K31/00,A61K39/02,A61K39/17,A61K39/215,
PC C07K34/125,
PC C07K14/165,C07K14/30,C12N7/00,C12N15/00
CC
CH Key Location/Qualifiers
FH source 1..101
FT /organism="Rous sarcoma virus".
FT Location/Qualifiers
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FT /mol_type="genomic DNA"
FT /db_xref="taxon:11896"

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QY 1 TTTAAGTCCTAGTCGATACATAAAGCGCAATTCACCAATTCACCAATTCGTTGTCAC 60
Db TTTAAGTCCTAGTCGATACATAAAGCGCAATTCACCAATTCACCAATTCGTTGTCAC 91
QY 61 CTC 63
Db 92 CTC 94
RESULT 2
LOCUS AX175190 648 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 1 from Patent WO0142444.
ACCESSION AX175190
VERSION AX175190.1 GI:14598581
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Rivera,V., Zoltick,P. and Wilson,J.M.
TITLE Methods for expression of genes in primates
JOURNAL Patent: WO 0142444-A 1 14-JUN-2001;
ARIAD GENE THERAPEUTICS, INC. (US); THE UNIVERSITY OF PENNSYLVANIA (US)
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source Location/Qualifiers
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/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="vector/RSV promoter/vector"
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Best Local Similarity 100.0%; Pred.No.1.5e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 550 TTTAAGTCCTAGTCGATACATAAAGCGCAATTCACCAATTCACCAATTCGTTGTCAC 609
QY 61 CTC 63
Db 610 CTC 612
RESULT 3
LOCUS AX175195 648 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 6 from Patent WO0142444.
ACCESSION AX175195
VERSION AX175195.1 GI:14598586
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Rivera,V., Zoltick,P. and Wilson,J.M.
TITLE Methods for expression of genes in primates
JOURNAL Patent: WO 0142444-A 6 14-JUN-2001;
ARIAD GENE THERAPEUTICS, INC. (US); THE UNIVERSITY OF PENNSYLVANIA (US)
FEATURES
source Location/Qualifiers
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/mol_type="synthetic construct"
/db_xref="taxon:32630"

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/note="MluI/RSV promoter/BglI"

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Query Match 100.0%; Score 63; DB 6; Length 648;
 Best Local Similarity 100.0%; Pred. No. 1.5e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
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 Db 550 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 609
 |||||

QY 61 CTC 63
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 Db 610 CTC 612

RESULT 4

EVU67090 2309 bp mRNA linear SYN 29-OCT-2001
 DEFINITION Expression vector pNEX2 beta-lactamase mRNA, complete cds.
 ACCESSION U67090
 VERSION U67090.1 GI:1561767
 KEYWORDS Expression vector pNEX2
 SOURCE Expression vector pNEX2
 ORGANISM artificial sequences; vectors.

REFERENCE 1 (bases 1 to 2309)
 Kaang,B.K.
 TITLE Parameters influencing ectopic gene expression in Aplysia neurons
 JOURNAL Neurosci. Lett. 221 (1), 29-32 (1996)
 MEDLINE 97166442
 PUBMED 9014173
 REFERENCE 2 (bases 1 to 2309)
 Kaang,B.-K.
 TITLE Direct Submission
 JOURNAL Submitted (16-AUG-1996) Inst. for Mol. Biol. & Genet., Seoul
 National University, San 56-1, Silim-dong, Kwanak-gu, Seoul
 151-742, Korea

FEATURES

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 9..15
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 17..103
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 107..169
 /notes="polylinker region from pUC19"
 190..331
 /notes="polyadenylation signal sequence from simian virus 40"

CDS

454..1314
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 /note="selection marker"
 /codon_start=1
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 IELDLSKILSPERPERFPMSTFKVLICGAVLSRIDAGQQLGRIRHYSDNLEVE
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 DRWPELNEAIENDRDTTPVAMATTKLTGELLTGLASRQLIDWMEADKVGPL
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 2073..2309
 /note="ColEI origin of replication from pUC19"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
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QY 61 CTC 63
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 Db 103 CTC 105

RESULT 5

EVU51722 2794 bp DNA circular SYN 14-SEP-1996
 LOCUS Expression vector pNEX delta, complete sequence.
 DEFINITION
 ACCESSION U51722
 VERSION U51722.1 GI:1277160
 KEYWORDS Expression vector pNEX delta
 SOURCE Expression vector pNEX delta
 ORGANISM artificial sequences; vectors.

REFERENCE 1 (sites)
 Kaang,B.K., Kandel,E.R. and Grant,S.G.
 TITLE Activation of cAMP-responsive genes by stimuli that produce
 long-term facilitation in Aplysia sensory neurons
 JOURNAL Neuron 10 (3), 427-435 (1993)
 MEDLINE 93213500
 PUBMED 8384857
 REFERENCE 2 (bases 1 to 2794)
 Kaang,B.-K.
 TITLE Direct Submission
 JOURNAL Submitted (19-MAR-1996) Bong-Kiun Kaang, Seoul National University,
 Inst. for Mol. Biol. & Genet., San 56-1, Silim-dong, Kwanak-gu,
 Seoul, Korea, 151-742

FEATURES

Location/Qualifiers

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 /db_xref="taxon:51098"
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 /bound_moiety="AP-1 protein"
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 89..176
 /note="minimal promoter from RSV LTR for transcription"
 /evidence=experimental
 180..242
 /note="polylinker region from pUC19, pNEXdelta derived
 from pNEX to generate two more cloning sites, HindIII and
 PvuII"
 /function="multiple cloning sites"
 /evidence=experimental
 551..682
 /note="polyadenylation signal sequences from simian virus
 40"

polyA_signal

551..682
 /note="polyadenylation signal sequences from simian virus
 40"

CDS

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rep_origin

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Query Match 100.0%; Score 63; DB 12; Length 2309;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
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QY 61 CTC 63
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Db 176 CTC 178

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LOCUS      Expression vector pNEX delta F, complete sequence.
DEFINITION      AY229985
ACCESSION      AY229985
VERSION      AY229985.1 GI:29469036
KEYWORDS
SOURCE      Expression vector pNEX delta F
ORGANISM      Expression vector pNEX delta F
artificial sequences; vectors.
REFERENCE      1 (bases 1 to 2856)
AUTHORS      Lee, Y., Han, J.-H., Lim, C.-S., Chang, D.-J., Lee, Y.-S., Soh, H., Park, C.-S.
              and Kaang, B.-K.
TITLE      Impairment of a parabolic bursting rhythm by the ectopic expression
              of a small conductance Ca(2+)-activated K(+) channel in Aplysia
              neuron R15
JOURNAL      Neurosci. Lett. 349 (1), 53-57 (2003)
MEDLINE      22827995
PubMed      12946595
REFERENCE      2 (bases 1 to 2856)
AUTHORS      Lee, Y., Han, J.-H., Lim, C.-S., Chang, D.-J., Lee, Y.-S., Park, C.-S.
              and Kaang, B.-K.
TITLE      Direct Submission
JOURNAL      Submitted (04-FEB-2003) School of Biological Science, Seoul
              National University, San56-1 Silim-dong Kwanak-gu, Seoul 151-742,
              Korea
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    LRSALFAGWFIADKSGAGERSGRIIAALGPDGKPSRIIVYITGSOATMDERNRQIA
    EIGASLIKHW"
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    LOCUS      EVU51721      2981 bp      DNA      circular SYN 17-SEP-1996
    DEFINITION      Expression vector pNEX, complete sequence.
    ACCESSION      U51721
    VERSION      U51721.1 GI:1277158
    KEYWORDS
    SOURCE      Expression vector pNEX
    ORGANISM      Expression vector pNEX
    artificial sequences, vectors.
    REFERENCE      1 (bases 1 to 2981)

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QY 61 CTC 63
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Db 176 CTC 178

RESULT 7
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LOCUS      Expression vector pNEX delta R, complete sequence.
DEFINITION      AY229986
ACCESSION      AY229986
VERSION      AY229986.1 GI:29423755
KEYWORDS
SOURCE      Expression vector pNEX delta R
ORGANISM      Expression vector pNEX delta R
artificial sequences; vectors.
REFERENCE      1 (bases 1 to 2895)
AUTHORS      Lee, Y.-S. and Kaang, B.-K.
TITLE      Direct Submission
JOURNAL      Submitted (04-FEB-2003) School of Biological Science, Seoul
              National University, San 56-1 Silim-dong Kwanak-gu, Seoul 151-742,
              Korea
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    EIGASLIKHW"
    ORIGIN
    EVU51721
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    DEFINITION      Expression vector pNEX, complete sequence.
    ACCESSION      U51721
    VERSION      U51721.1 GI:1277158
    KEYWORDS
    SOURCE      Expression vector pNEX
    ORGANISM      Expression vector pNEX
    artificial sequences, vectors.
    REFERENCE      1 (bases 1 to 2981)

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AUTHORS Kaang,B.-K., Pfaffinger,P.J., Grant,S.G., Kandel,E.R. and Furukawa,Y.
TITLE Overexpression of an Aplysia shaker K⁺ channel gene modifies the electrical properties and synaptic efficacy of identified Aplysia neurons
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (3), 1133-1137 (1992)
MEDLINE 92141216
PUBMED 1310540
REFERENCE 2 (bases 1 to 2981)
AUTHORS Kaang,B.-K.
TITLE Neuronal expression of reporter genes in the intact nervous system of Aplysia
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2981)
AUTHORS Kaang,B.-K.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1996) Bong-Kiun Kaang, Seoul National University, Inst. for Mol. Biol. & Genet., San 56-1, Sillim-dong, Kwanak-gu, Seoul, Korea, 151-742
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 rep_origin
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ORIGIN
 Query Match 100.0%; Score 63; DB 12; Length 2981;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTGATACATAAAGCCATTGACCATTCACCATGCTGTGCAC 60
 Db 125 TTTAAGTCCTAGCTGATACATAAAGCCATTGACCATTCACCATGCTGTGCAC 184
 QY 61 CTC 63
 Db 185 CTC 187
RESULT 9
EVJ67091
LOCUS Expression vector pNEX3 beta-lactamase mRNA, complete cds.
DEFINITION Expression vector pNEX3 beta-lactamase mRNA, complete cds.

ACCESSION U67091
VERSION U67091.1 GI:1561769
KEYWORDS Expression vector pNEX3
SOURCE Expression vector pNEX3
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 3059)
AUTHORS Kaang,B.-K.
TITLE Parameters influencing ectopic gene expression in Aplysia neurons
JOURNAL Neurosci. Lett. 221 (1), 29-32 (1996)
MEDLINE 97166442
PUBMED 9014173
REFERENCE 2 (bases 1 to 3059)
AUTHORS Kaang,B.-K.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1996) Inst. for Mol. Biol. & Genet., Seoul National University, San 56-1, Sillim-dong, Kwanak-gu, Seoul 151-742, Korea
FEATURES
 Location/Qualifiers
 1..3059
 /organism="Expression vector pNEX3"
 /mol_type="mRNA"
 /db_xref="taxon:51681"
 /note="neuronal expression vector"
 16..160
 /note="eight copies of AP-1 binding site; four copies of AP-1 site inserted into pNEX, GenBank Accession Number U51721"
 /bound_moiety="AP-1"
 180..263
 /note="minimal promoter from RSV LTR for transcription"
 267..323
 /note="polylinker region from pUC19"
 637..770
 /note="polyadenylation signal sequence from simian virus 40"
 1026..1886
 /function="ampicillin resistance"
 /note="selection marker"
 /codon_start=1
 /product="beta-lactamase"
 /protein_id="AAB08872.1"
 /db_xref="GI:1561770"
 /translation="MSIQHFRVALIPFFAFCPLPVFAHPETLVKVKDAEDQLGARVGY
 IELDNLSKILLESFRRPEFRPMWSTFKVLGGAVLSRIDAGQQLGRIRHYSQNDLVE
 YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGPKELTAFLNNMGSHVTRL
 DRWPEELNEALPNDERDTMPVAVATTAKLTGELLTLASRQQLIDWVADKVGAGPL
 LRSALPAGWFIADKSGAGERSGRIIAALGPDGKFSRIWVYITGSGQATMDERNRQIA
 EIGASLIKHWH"
 rep_origin
 2645..3059
 /note="ColE1 origin of replication from pUC19"
ORIGIN
 Query Match 100.0%; Score 63; DB 12; Length 3059;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTGATACATAAAGCCATTGACCATTCACCATGCTGTGCAC 60
 Db 203 TTTAAGTCCTAGCTGATACATAAAGCCATTGACCATTCACCATGCTGTGCAC 262
 QY 61 CTC 63
 Db 263 CTC 265
RESULT 10
A30504
LOCUS A30504
DEFINITION Plasmid p79DBAM.
ACCESSION A30504
VERSION A30504.1 GI:23957133
KEYWORDS

```

SOURCE      synthetic construct
ORGANISM     synthetic construct
            artificial sequences.
REFERENCE    1 (bases 1 to 3189)
AUTHORS      Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE        Soluble interferon-gamma receptors and methods for their production
JOURNAL      Patent: EP 0393502-A 71 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES     Location/Qualifiers
            source
            1..3189
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 3189;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 60
        |||||||
Db      251 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 310
QY      61 CTC 63
        |||
Db      311 CTC 313

RESULT 11
A30505
LOCUS      A30505      3277 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p238BGL.
ACCESSION  A30505
VERSION     A30505.1 GI:23957134
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM   1 (bases 1 to 3277)
REFERENCE  1 (bases 1 to 3277)
AUTHORS    Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE      Soluble interferon-gamma receptors and methods for their production
JOURNAL    Patent: EP 0393502-A 72 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES   Location/Qualifiers
            source
            1..3277
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 3277;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 60
        |||||||
Db      251 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 310
QY      61 CTC 63
        |||
Db      311 CTC 313

RESULT 12
A30507
LOCUS      A30507      3277 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p238BAM.
ACCESSION  A30507
VERSION     A30507.1 GI:23957135
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM   1 (bases 1 to 3427)
REFERENCE  1 (bases 1 to 3427)
AUTHORS    Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE      Soluble interferon-gamma receptors and methods for their production
JOURNAL    Patent: EP 0393502-A 74 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES   Location/Qualifiers
            source
            1..3427
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 3427;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 60
        |||||||
Db      251 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 310
QY      61 CTC 63
        |||
Db      311 CTC 313

RESULT 13
A30503
LOCUS      A30503      3384 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p79BGL.
ACCESSION  A30503
VERSION     A30503.1 GI:23957132
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM   1 (bases 1 to 3384)
REFERENCE  1 (bases 1 to 3384)
AUTHORS    Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE      Soluble interferon-gamma receptors and methods for their production
JOURNAL    Patent: EP 0393502-A 69 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES   Location/Qualifiers
            source
            1..3384
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 3384;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 60
        |||||||
Db      251 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 310
QY      61 CTC 63
        |||
Db      311 CTC 313

RESULT 14
A30513
LOCUS      A30513      3427 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p267BGL.
ACCESSION  A30513
VERSION     A30513.1 GI:23957138
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM   1 (bases 1 to 3427)
REFERENCE  1 (bases 1 to 3427)
AUTHORS    Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE      Soluble interferon-gamma receptors and methods for their production
JOURNAL    Patent: EP 0393502-A 74 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES   Location/Qualifiers
            source
            1..3427
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
ORIGIN

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REFERENCE    1 (bases 1 to 3277)
AUTHORS      Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE        Soluble interferon-gamma receptors and methods for their production
JOURNAL      Patent: EP 0393502-A 74 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES     Location/Qualifiers
            source
            1..3277
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 3277;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 60
        |||||||
Db      251 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 310
QY      61 CTC 63
        |||
Db      311 CTC 313

RESULT 13
A30503
LOCUS      A30503      3384 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p79BGL.
ACCESSION  A30503
VERSION     A30503.1 GI:23957132
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM   1 (bases 1 to 3384)
REFERENCE  1 (bases 1 to 3384)
AUTHORS    Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE      Soluble interferon-gamma receptors and methods for their production
JOURNAL    Patent: EP 0393502-A 69 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES   Location/Qualifiers
            source
            1..3384
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 3384;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 60
        |||||||
Db      251 TTTAAGTGCCTAGCTCGATACATAAAGCCGCAATTTGACCATTCACCACTTGGTGTGCAC 310
QY      61 CTC 63
        |||
Db      311 CTC 313

RESULT 14
A30513
LOCUS      A30513      3427 bp      DNA      linear      PAT 05-JUL-2002
DEFINITION Plasmid p267BGL.
ACCESSION  A30513
VERSION     A30513.1 GI:23957138
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM   1 (bases 1 to 3427)
REFERENCE  1 (bases 1 to 3427)
AUTHORS    Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE      Soluble interferon-gamma receptors and methods for their production
JOURNAL    Patent: EP 0393502-A 74 24-OCT-1990;
            F. HOFFMANN-LA ROCHE AG
FEATURES   Location/Qualifiers
            source
            1..3427
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
ORIGIN

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JOURNAL Patent: EP 0393502-A 80 24-OCT-1990;
FEATURES F. HOFFMANN-LA ROCHE AG
SOURCE location/Qualifiers
1..3427
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 3427;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
DB 250 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 309

QY 61 CTC 63
DB 310 CTC 312

RESULT 15
A30515
LOCUS Plasmid p267BAM. 3427 bp DNA linear PAT 05-JUL-2002
DEFINITION A30515
ACCESSION A30515
VERSION A30515.1 GI:23957139
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 3427)
AUTHORS Fountoulakis M., Garotta, G. and Stueber, D.
TITLE Soluble interferon-gamma receptors and methods for their production
JOURNAL Patent: EP 0393502-A 82 24-OCT-1990;
F. HOFFMANN-LA ROCHE AG
FEATURES location/Qualifiers
1..3427
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 3427;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
DB 250 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 309

QY 61 CTC 63
DB 310 CTC 312

RESULT 16
SYNRSV3MV
LOCUS Cloning vector RSV3. 3557 bp DNA circular SYN 27-APR-1993
DEFINITION M83240
ACCESSION M83240
VERSION M83240.1 GI:209303
KEYWORDS cDNA expression vector.
SOURCE unidentified cloning vector
ORGANISM unidentified cloning vector
artificial sequences; vectors.
REFERENCE 1 (sites)
AUTHORS Messing, J.
TITLE New M13 vectors for cloning
JOURNAL Meth. Enzymol. 101, 20-78 (1983)
MEDLINE 83296918
PUBMED 6310323

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REFERENCE 2 (sites)
AUTHORS Gorman, C., Padmanabhan, R. and Howard, B.H.
TITLE High efficiency DNA-mediated transformation of primate cells
JOURNAL Science 221 (4610), 551-553 (1983)
MEDLINE 83249156
PUBMED 6306768
REFERENCE 3 (bases 1 to 3557)
AUTHORS Jacobson, S., Sekaly, R.P., Jacobson, C.L., McFarland, H.F. and Long, E.O.
TITLE HLA class II-restricted presentation of cytoplasmic measles virus antigens to cytotoxic T cells
JOURNAL J. Virol. 63 (4), 1756-1762 (1989)
MEDLINE 89178863
PUBMED 2784508
COMMENT Original source text: Cloning vector DNA.
FEATURES location/Qualifiers
1..3557
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
misc_feature 1..29
/function="polylinker"
/evidence=experimental
misc_feature 912..3029
/function="ampicillin-resistance, replication origin"
/evidence=experimental
enhancer 3030..3557
/standard_name="5'LTR of Rous Sarcoma Virus"
/citations[2]
/evidence=experimental
ORIGIN
Query Match 100.0%; Score 63; DB 12; Length 3557;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
DB 3491 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 3550

QY 61 CTC 63
DB 3551 CTC 3553

RESULT 17
A30511
LOCUS Plasmid p264BAM. 3979 bp DNA linear PAT 05-JUL-2002
DEFINITION A30511
ACCESSION A30511
VERSION A30511.1 GI:23957137
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 3979)
AUTHORS Fountoulakis, M., Garotta, G. and Stueber, D.
TITLE Soluble interferon-gamma receptors and methods for their production
JOURNAL Patent: EP 0393502-A 78 24-OCT-1990;
F. HOFFMANN-LA ROCHE AG
FEATURES location/Qualifiers
1..3979
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 3979;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60

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Db 250 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 309
QY 61 CTC 53
Db 310 CTC 312

RESULT 18
A30509
LOCUS A30509 3980 bp DNA linear PAT 05-JUL-2002
DEFINITION Plasmid p264BGL.
ACCESSION A30509
VERSION A30509.1 GI:23957136
KEYWORDS synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 3980)
AUTHORS Fountoulakis,M., Garotta,G. and Stueber,D.
TITLE Soluble interferon-gamma receptors and methods for their production
JOURNAL Patent: EP 0395502-A 76 24-OCT-1990;
F. HOFFMANN-LA ROCHE AG
FEATURES
source Location/Qualifiers
1..3980
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 3980;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 60
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Db 251 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 310
QY 61 CTC 53
Db 311 CTC 313

RESULT 19
AR071324/c
LOCUS AR071324 4059 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 2 from patent US 5910488.
ACCESSION AR071324
VERSION AR071324.1 GI:722212
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4059)
AUTHORS Nabel,G.J., Nabel,E.G., Lew,D. and Marquet,M.
TITLE Plasmids suitable for gene therapy
JOURNAL Patent: US 5910488-A 2 08-JUN-1999;
F. Hoffmann-LA Roche AG
FEATURES
source Location/Qualifiers
1..4059
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 4059;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 60
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Db 2954 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 2895
QY 61 CTC 53
Db 2894 CTC 2892

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RESULT 20
A38214
LOCUS A38214 4341 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 58 from Patent WO9408008.
ACCESSION A38214
VERSION A38214.1 GI:2294819
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4341)
AUTHORS Hawkins,R.E., Russell,S.J., Stevenson,F.K. and Winter,G.P.
TITLE IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
JOURNAL Patent: WO 9408008-A 58 14-APR-1994;
MEDICAL RES COUNCIL (GB)
COMMENT Other publication CA 2145064 940414
Other publication AU 4832493 940426
Other publication JP 8501699T 960227.
FEATURES
source Location/Qualifiers
1..4341
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 4341;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 60
|||||
Db 542 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 601
QY 61 CTC 53
Db 602 CTC 604

RESULT 21
AX286570
LOCUS AX286570 4341 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 1 from Patent WO0179510.
ACCESSION AX286570
VERSION AX286570.1 GI:17048664
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Rice,J.H. and Stevenson,F.M.
TITLE Materials and methods relating to immune responses to fusion
PROTEINS
JOURNAL Patent: WO 0179510-A 1 25-OCT-2001;
Cancer Research Ventures Limited (GB)
FEATURES
source Location/Qualifiers
1..4341
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Vector pVAC1"
ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 4341;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 60
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Db 542 TTTAAGTGCCTAGCTCGATACATAAAAGCCATTGGACCATTCACCACTTGGTGTGCAC 601
QY 61 CTC 53

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Db          602 CTC 604
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RESULT 22
AX743954
LOCUS      AX743954          4457 bp      DNA      linear      PAT 14-MAY-2003
DEFINITION Sequence 2 from Patent WO03031630.
ACCESSION  AX743954
VERSION     AX743954.1 GI:30722651
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Pazio, V., Rinaldi, M., Sonzogni, L., Tonon, G. and Orsini, G.
TITLE       Multi-cisronic vectors for gene transfer protocols
JOURNAL     Patent: WO 03031630-A 2 17-APR-2003;
            Keryos Spa (IT)
FEATURES   Location/Qualifiers
            source
            1..4457
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 4457;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAACGCCATTTCACCATTCACCATTCGGTGTGCAC 60
|||||
Db 918 TTTAAGTCCTAGCTCGATACAAATAACGCCATTTCACCATTCACCATTCGGTGTGCAC 977
|||||

QY 61 CTC 63
|||||
Db 978 CTC 980
|||||

RESULT 23
SYNRSV5GPT
LOCUS      SYNRSV5GPT          4839 bp      DNA      circular SYN 16-MAR-2000
DEFINITION Cloning vector RSV.5(gpt).
ACCESSION  M83236
VERSION     M83236.1 GI:209304
KEYWORDS   cDNA expression vector.
SOURCE      Cloning vector pUC19
ORGANISM    Cloning vector pUC19
            artificial sequences; vectors.
REFERENCE   1 (bases 1 to 4839)
AUTHORS     Long, E.O., Rosen-Bronson, S., Karp, D.R., Malnati, M., Sekaly, R.P. and
            Jaraquemada, D.
TITLE       Efficient cDNA expression vectors for stable and transient
            expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL     Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE    92011006
PUBMED     1655683
FEATURES   Location/Qualifiers
            source
            1..4839
            /organism="Cloning vector pUC19"
            /mol_type="genomic DNA"
            /db_xref="taxon:31851"
            /focus
            1..29
            /organism="Cloning vector pUC12"
            /mol_type="genomic DNA"
            /db_xref="taxon:83674"
            /note="HindIII to BamHI fragment of pUC12"
            30..872
            /organism="Simian virus 40"
            /mol_type="genomic DNA"
            /db_xref="taxon:10633"
            /note="Bi-directional SV40 termination and

poly-adenylation sequences."
873..1929
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
1930..2273
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/note="SV40 early promoter and origin of replication."
2274..4311
/organism="Cloning vector pBR322"
/mol_type="genomic DNA"
/db_xref="taxon:47470"
/note="Ampicillin resistance gene and origin of replication
from the vector pBR322."
4312..4839
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11886"
/note="5' long terminal repeat."
1..29
/function="polylinker"
/evidence=experimental
misc_feature complement (873..1929)
/product="guanine-hypoxanthine phosphoribosyltransferase"
/standard_name="gpt"
/note="gpt gene from E.coli, putative mature peptide -
contains internal stop codons; putative"
2274..4311
/function="ampicillin resistance and origin of
replication"
/evidence=experimental

ORIGIN
Query Match      100.0%; Score 63; DB 12; Length 4839;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACAAATAACGCCATTTCACCATTCACCATTCGGTGTGCAC 60
|||||
Db 4773 TTTAAGTCCTAGCTCGATACAAATAACGCCATTTCACCATTCACCATTCGGTGTGCAC 4832
|||||

QY 61 CTC 63
|||||
Db 4833 CTC 4835
|||||

RESULT 24
SYNRSV5NEO
LOCUS      SYNRSV5NEO          5108 bp      DNA      linear      SYN 06-APR-2001
DEFINITION cDNA expression vector RSV.5(neo).
ACCESSION  M83237
VERSION     M83237.1 GI:209305
KEYWORDS   cDNA expression vector.
SOURCE      Expression vector RSV.5(neo)
ORGANISM    Expression vector RSV.5(neo)
            artificial sequences; vectors.
REFERENCE   1 (bases 1 to 5108)
AUTHORS     Long, E.O., Rosen-Bronson, S., Karp, D.R., Malnati, M., Sekaly, R.P. and
            Jaraquemada, D.
TITLE       Efficient cDNA expression vectors for stable and transient
            expression of HLA-DR in transfected fibroblast and lymphoid cells
JOURNAL     Hum. Immunol. 31 (4), 229-235 (1991)
MEDLINE    92011006
PUBMED     1655683
FEATURES   Location/Qualifiers
            source
            1..5108
            /organism="Expression vector RSV.5(neo)"
            /mol_type="genomic DNA"
            /db_xref="taxon:118308"
            /focus
            1..29
            /organism="Expression vector RSV.5(neo)"
            /mol_type="genomic DNA"
            /db_xref="taxon:118308"
            /focus
            1..29

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/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/noife="hindIII to BamHI fragment of pUC12."
30..872
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/noife="5'-directional SV40 termination and poly-adenylation sequence."
873..879
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/noife="Remnant of gpt gene from the cDNA expression vector RSV.5(gpt)."
880..2197
/organism="Cloning vector pSV2neo"
/mol_type="genomic DNA"
/db_xref="taxon:31846"
/noife="TN5 neomycin-resistance gene from cloning vector pSV2neo."
2198..2542
/organism="Simian virus 40"
/mol_type="genomic DNA"
/db_xref="taxon:10633"
/noife="SV40 early promoter and origin of replication."
2543..4580
/organism="Cloning vector pBR322"
/mol_type="genomic DNA"
/db_xref="taxon:47470"
/noife="Ampicillin resistance gene and origin of replication from pBR322."
4581..5108
/organism="Rous sarcoma virus"
/mol_type="genomic DNA"
/db_xref="taxon:11886"
/noife="5' long terminal repeat of Rous Sarcoma virus."
5109..5180
/function="polylinker"
/evidence="experimental"
/complement(880..2197)
/notes="neomycin resistance gene from pSV2neo, putative mature peptide - contains internal stop codons; putative"
2543..4580
/product="ampicillin resistance"
/function="ampicillin resistance and origin of replication"
/evidence="experimental"
4581..5108
/standard_name="5' LTR of Rous Sarcoma Virus"
/function="promoter"
/evidence="experimental"

ORIGIN
Query Match 100.0%; Score 63; DB 12; Length 5108;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGACCATTCACCATTCGGTGTGCAC 60
|||||
Db 5042 TTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGACCATTCACCATTCGGTGTGCAC 5101

Qy 61 CTC 63
|||
Db 5102 CTC 5104

RESULT 25
SYNCRS
LOCUS 5564 bp DNA linear SYN 27-SEP-1994
DEFINITION Cloning vector murine T-cell receptor C-beta 1 DNA, 3' end of cds.
ACCESSION L36555

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L36555.1 GI:550523
T-cell receptor C-beta 1; T-cell receptor V-beta; cloning vector.
unidentified cloning vector
unidentified cloning vector
artificial sequences; vectors.
1 (bases 1 to 5564)
Palmer, M.S., Bentley, A., Gould, K. and Townsend, A.R.
The T cell receptor from an influenza-A specific murine CTL clone
Nucleic Acids Res. 17 (6), 2353 (1989)
89202046
MEDLINE
PUBMED 2784852
2 (bases 1 to 5564)
Long, E.O., Rosen-Bronson, S., Karp, D.R., Malnati, M., Sekaly, R.P. and
Jaraquemada, D.
Efficient cDNA expression vectors for stable and transient
expression of HLA-DR in transfected fibroblast and lymphoid cells
Hum. Immunol. 31 (4), 229-235 (1991)
92011006
PUBMED 1655683
3 (bases 1 to 5564)
Denis, P., Soudeyria, H., Ringnette, N. and Sekaly, R.-P.
A simple method for the cloning and functional expression of human
T cell receptor Vbeta segments in murine hybridomas
Unpublished (1994)
Original source text: Cloning vector DNA.
Location/Qualifiers
1..5564
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
<13..480
/notes="murine"
/citation=[3]
/codon_start=1
/evidence="experimental"
/transl_table=11
/product="T-cell receptor C beta 1"
/protein_id="AAA72448.1"
/db_xref="GI:550524"
/transl_table="VDIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQA
YKESNYVCLSRLEVSATFNHPRHFCOVQPHGLSEEDKWPGEKPKPTQNISAE
AWGRDQGTSSHQVLSATILVEILLKATILYAVLSGLVLMVYKKNS"

ORIGIN
Query Match 100.0%; Score 63; DB 12; Length 5564;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGACCATTCACCATTCGGTGTGCAC 60
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Db 5498 TTTAAGTGCCTAGCTCGATACAAATAAAGCCATTGACCATTCACCATTCGGTGTGCAC 5557

Qy 61 CTC 63
|||
Db 5558 CTC 5560

RESULT 26
LOCUS 5564 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5650306.
ACCESSION 156772
VERSION 156772.1 GI:2477185
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5653)
AUTHORS Nabel, G.J., Yang, Z.-Y., Liu, J. and Woffendin, C.
TITLE Recombinant nucleic acids for inhibiting HIV gene expression
JOURNAL Patent: US 5650306-A 3 22-JUL-1997;
FEATURES Location/Qualifiers
1..5653

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into Mammalian Cells
DATE 06-JUN-1986
#sequence 16-DEC-1986
ACCESSION VB0064
SOURCE artificial
COLLECTION ATCC 37198
REFERENCE
#number 1
#authors Gorman C.
#book 'DNA cloning Volume II, a practical approach', pp.
143-190,
edited by D. M. Glover, IRL Press, (1986),
eds. D. Rickwood and B. D. Hames
COMMENT
Entered by William Gilbert, Whitaker College, MIT, 02-APR-1986
Revised 16-DEC-1986 by F. Pfeiffer:
1012/3 'AT' to 'TA' to match revised sequence of PBR322 KEYWORDS
CROSSREFERENCE
#parent
VecBase(3):PBR322, GenBank(50):SV4CG,
GenBank(50):ALRPROLTH,
GenBank(50):Trn5Neo, GenBank(50):Trn5IR1
PARENT
Features of pRSVNeo (5736 bp)
residue source
6-529 550- 27 (c) Rous Sarcoma Virus (GenBank(50):
ALRPROLTH)
6- 529 3189-2667 (c) GenBank(50):ALRPROLTH (6 mutations)
529-2644 2248-4363 PBR322
2641-3634 1781-2774 SV40
3631-4244 4100-4713 SV40
4248-5533 1286- 1 (c) Trn5 (GenBank(50):Trn5Neo)
5251-5736 1720-1235 (c) Trn5 (GenBank(50):Trn5IR1)
Conflict (cfl) and Mutations (mut): none
FEATURE
1579-2367 789-1 (c) Ap-R; b-lactamase
4589-5383 791-1 (c) Neo-R
POLYLINKER
SELECTION #resistance Ap
SUMMARY pRSVNeo #length 5736 #checksum 3569.
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source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 100.0%; Score 63; DB 12; Length 5736;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATGTTGTGCAC 60
Db 67 TTTAAGTCCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATGTTGTGCAC 8
QY 61 CTC 63
Db 7 CTC 5
RESULT 29
AR215114
LOCUS
DEFINITION
ACCESSION
VERSION AR215114.1 GI:23319242
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 6836)
Harrington,J.J. and Rundlett,S.
Compositions and methods for non-targeted activation of endogenous
into Mammalian Cells
DATE 06-JUN-1986
#sequence 16-DEC-1986
ACCESSION VB0064
SOURCE artificial
COLLECTION ATCC 37198
REFERENCE
#number 1
#authors Gorman C.
#book 'DNA cloning Volume II, a practical approach', pp.
143-190,
edited by D. M. Glover, IRL Press, (1986),
eds. D. Rickwood and B. D. Hames
COMMENT
Entered by William Gilbert, Whitaker College, MIT, 02-APR-1986
Revised 16-DEC-1986 by F. Pfeiffer:
1012/3 'AT' to 'TA' to match revised sequence of PBR322 KEYWORDS
CROSSREFERENCE
#parent
VecBase(3):PBR322, GenBank(50):SV4CG,
GenBank(50):ALRPROLTH,
GenBank(50):Trn5Neo, GenBank(50):Trn5IR1
PARENT
Features of pRSVNeo (5736 bp)
residue source
6-529 550- 27 (c) Rous Sarcoma Virus (GenBank(50):
ALRPROLTH)
6- 529 3189-2667 (c) GenBank(50):ALRPROLTH (6 mutations)
529-2644 2248-4363 PBR322
2641-3634 1781-2774 SV40
3631-4244 4100-4713 SV40
4248-5533 1286- 1 (c) Trn5 (GenBank(50):Trn5Neo)
5251-5736 1720-1235 (c) Trn5 (GenBank(50):Trn5IR1)
Conflict (cfl) and Mutations (mut): none
FEATURE
1579-2367 789-1 (c) Ap-R; b-lactamase
4589-5383 791-1 (c) Neo-R
POLYLINKER
SELECTION #resistance Ap
SUMMARY pRSVNeo #length 5736 #checksum 3569.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATGTTGTGCAC 60
Db 542 TTTAAGTCCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATGTTGTGCAC 601
QY 61 CTC 63
Db 602 CTC 604
RESULT 27
I95540
LOCUS
DEFINITION
ACCESSION
VERSION I95540.1 GI:3940010
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 5653)
Nabel,G.J., Woffendin,C., Yang,N.-S. and Sheehy,M.J.
Introduction of HIV-protective genes into cells by
particle-mediated gene transfer
Patent: US 5733543-A 1 31-MAR-1998;
Location/Qualifiers
1..5653
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 5653;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATGTTGTGCAC 60
Db 542 TTTAAGTCCTAGCTCGATACAAATAAAGCCATTGACCAATTCACCAATGTTGTGCAC 601
QY 61 CTC 63
Db 602 CTC 604
RESULT 28
SYNPRSVNeo/c
LOCUS
DEFINITION
ACCESSION
VERSION SYNPRSVNeo 5736 bp DNA circular SYN 27-APR-1993
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 5736)
Gilbert,W.
Obtained from VecBase 3.0
Unpublished (1991)
Original source text: Synthetic construct DNA.
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. pRSVNeo
- Cloning Vector for High Efficiency Gene Transfer into Mammalian
Cells
ENTRY PRSVNeo #TYPE DNA CIRCULAR TITLE PRSVNeo -
Cloning Vector for High Efficiency Gene Transfer

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genes
JOURNAL Patent: US 6410266-A 18 25-JUN-2002;
FEATURES   Location/Qualifiers
   source   1..6836
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
    |||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
    |||
Db 1820 CTC 1822

RESULT 30
AR302356 AR302356 6836 bp DNA linear PAT 12-JUN-2003
LOCUS     Sequence 18 from patent US 6541221.
ACCESSION AR302356
VERSION   AR302356.1 GI:31690610
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS  Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE     Compositions and methods for non-targeted activation of endogenous
          genes
JOURNAL   Patent: US 6541221-A 18 01-APR-2003;
FEATURES   Location/Qualifiers
   source   1..6836
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            /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
    |||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
    |||
Db 1820 CTC 1822

RESULT 31
AR373228 AR373228 6836 bp DNA linear PAT 18-DEC-2003
LOCUS     Sequence 18 from patent US 6602686.
ACCESSION AR373228
VERSION   AR373228.1 GI:40075236
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS  Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE     Compositions and methods for non-targeted activation of endogenous
          genes
JOURNAL   Patent: US 6602686-A 18 05-AUG-2003;
FEATURES   Location/Qualifiers
   source   1..6836
            /organism="unknown"

genes
JOURNAL Patent: US 6410266-A 18 25-JUN-2002;
FEATURES   Location/Qualifiers
   source   1..6836
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
    |||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
    |||
Db 1820 CTC 1822

RESULT 32
AR401614 AR401614 6836 bp DNA linear PAT 18-DEC-2003
LOCUS     Sequence 18 from patent US 6623958.
ACCESSION AR401614
VERSION   AR401614.1 GI:40149062
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 6836)
AUTHORS  Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE     Compositions and methods for non-targeted activation of endogenous
          genes
JOURNAL   Patent: US 6623958-A 18 23-SEP-2003;
FEATURES   Location/Qualifiers
   source   1..6836
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 6836;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 60
    |||||
Db 1760 TTTAAGTGCTAGCTCGATACATAAAGCGCCATTGGACCATTCACACATTGGTGTGCAC 1819

Qy 61 CTC 63
    |||
Db 1820 CTC 1822

RESULT 33
AF346624 AF346624 6836 bp DNA circular SYN 30-AUG-2001
LOCUS     RAGE vector pRIG1, complete sequence.
ACCESSION AF346624
VERSION   AF346624.1 GI:15383987
KEYWORDS
SOURCE    RAGE vector pRIG1
ORGANISM  RAGE vector pRIG1
          artificial sequences; vectors.
REFERENCE 1 (bases 1 to 6836)
AUTHORS  Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
          Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
          Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Bozzer,S.,
          Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
          Offenbacher,J., Danzig,J. and Ducar,M.
          Creation of genome-wide protein expression libraries using random
          activation of gene expression
          Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL   21227151
MEDLINE   11329013
PUBMED
REFERENCE 2 (bases 1 to 6836)
AUTHORS  Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
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Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J.,
 Ierner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E.,
 Veloso, N., Hess, J., Cottrien, K., Lo, K., Offenbacher, J., Danzig, J.,
 and Ducar, M.
 Direct Submission
 Submitted (06-FEB-2001) Atherxsys, Inc., 3201 Carnegie Ave.,
 Cleveland, OH 44115, USA
 TITLE
 JOURNAL
 FEATURES
 source
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 /organism="BAGE vector pRIG1"
 /mol_type="genomic DNA"
 /db_xref="taxon:161236"
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
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 QY 1 TTTAAGTCCCTAGCTCGATACCAATAAAGCCGCAATTCACCAATTCACCAATTCGTCGAC 60
 Db 1760 TTTAAGTCCCTAGCTCGATACCAATAAAGCCGCAATTCACCAATTCACCAATTCGTCGAC 1819
 QY 61 CTC 63
 Db 1820 CTC 1822
 RESULT 34
 XXU19931
 LOCUS
 DEFINITION Cloning vector pGlaCRSV, 6864 bp DNA linear SYN 30-MAR-1995
 ACCESSION U19931
 VERSION U19931.1 GI:644834
 KEYWORDS
 SOURCE Cloning vector pGlaCRSV
 ORGANISM Cloning vector pGlaCRSV
 Cloning vector pGlaCRSV
 artificial sequences; vectors.
 REFERENCE
 1 (bases 1 to 6864)
 Gottgens, B.B.
 TITLE A versatile lacZ reporter vector
 JOURNAL Unpublished
 REFERENCE
 2 (bases 641 to 4011)
 Ravid, K., Beiler, D.L., Rabin, M.S., Ruley, H.E. and Rosenberg, R.D.
 TITLE Selective targeting of gene products with the megakaryocyte
 platelet factor 4 promoter
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1521-1525 (1991)
 MEDLINE 91142205
 PUBMED 1899930
 REFERENCE
 3 (bases 1 to 6864)
 Gottgens, B.B.
 TITLE Direct Submission
 JOURNAL Submitted (18-JAN-1995) Berthold B. Gottgens, Hematology, Cambridge
 University, MRC Centre, Hills Road, Cambridge, UK, CB2 2QH
 FEATURES
 Location/Qualifiers
 1..6864
 /organism="Cloning vector pGlaCRSV"
 /mol_type="genomic DNA"
 /db_xref="taxon:39038"
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 /note="obtained from pGlaC, Genbank Accession Number U19930"
 misc_feature 38..631
 /note="RSV LTR from pRC/RSV cloned as a BglII/HindIII fragment"
 misc_feature 632..6864
 /note="obtained from pGlaC, Genbank Accession Number U19930"
 misc_feature 641..4011
 /note="obtained from pSDXlacZpA containing the E. coli lacZ gene followed by an SV40 polyA site"
 /citation=[2]
 gene 662..3727
 /gene="lacZ"

662..3727
 /gene="lacZ"
 /codon_start=1
 /transl_table=11
 /product="b-galactosidase"
 /protein_id="AAA64569.1"
 /db_xref="GI:644835"
 /translation="MARDDPVVLORDWENPGVTOINRLAAHPFPAWSENSSEARTDR
 RSQQLRSINGENRPAWPAPEAVPESWLECDLPEADTVVVFESNWMQHGDAFIYTNVT
 YFITVNPFPVTENPTGCTISUTFNVDSEMLQEGQTRIIIFDGVNSAFHLMWQGRWVG
 QDSRLSEFDLSAFRAGENLAVMLRSDGSLYLEDQWMRMGIFRVDVSLHHPPT
 QISDFHATFNDPFRSLVLAELVQMGELRDLTVSLWQSGTVASGTAPFGGEI
 IDERGVDVRLRLNENPKLWSAETPNLXAVVELHSTADGTLIARAACDVGREVR
 IENGILLNGKPLLRINGVNRHEHPLHGOVMDQVQDILLKONNKNVPCSHYEN
 HPLWYTCDRYGLVVDZANIEHGMVFNRLTDDPRLPAMSERVTRVQVQDNHPS
 VLIISVNGSHGANDHAIKRWISVDPSPRQVQEGGADTTATDIIICPMYARVDDQ
 PFPAPKWSIKKWLILPGETRPILICBYAHAMGSLGGFAKYQAFQYPRIQGGFVW
 DWPDQSLIKYDENGNPWSAYGDEGTPNDQFCMNGLVFADRPALTEAKHQOOF
 FQFLSQITTEVSEYLFHNSDNLHWMVALDGKPLASGRVLDVAPQKOLIELPE
 LPQESAGOLMLTVRVPQNPATASEAGHISAQOQWPLAENLSVTLPAASHAIPLHT
 SEMDFCIELGNKQENQSGFSLQMWIGDKQLTLPDQFTRAPLDNDIGVSEATR
 IDPNARWKAAGHYQABALLOCTADTADAVLITTAHAWQHQKTLIFISERTYRI
 DSGQMAITVDVEVADTDFHARIGLNCQLAQAVRNVLGLGQENYEDRTAAACFD
 RWDLPLSDMYTPYVPSENGLRCGTRELNYPHWRGDFQENISYQQQLMETSHRH
 LLHAEGTWNIDGPHMGIGGDDSWSPSVSAEFQLSAGRHYQLVWCQK"
 4005..6864
 /note="vector backbone from pGI-2basic, Genbank Accession
 Number X65323"
 complement (5081..5941)
 /gene="bla"
 complement (5081..5941)
 /gene="bla"
 /codon_start=1
 /transl_table=11
 /product="beta-lactamase"
 /protein_id="AAA64570.1"
 /db_xref="GI:644836"
 /translation="MSIQHFRVALIPFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
 IELDNGSKILSEPRERFPEPMETKVLGKAVLSRIDAGQLGRIIRHYSQNDLVE
 YSPVTEKLDGMVRELCSAITMSDNTAANLLTTIGPKELTFLKRWGDDHVTSL
 DRWPELNEAIFNDERTIMEVAVATLRLKLLTGLLTLASRQQLLDWMEADKVAGPL
 LRSALPAGWFLDKSGAGERGRTIAALGPDGKFSRIWYITGTSQATMDERNQIA
 EIGASLIKHW"
 ORIGIN
 Query Match 100.0%; Score 63; DB 12; Length 6864;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCCTAGCTCGATACCAATAAAGCCGCAATTCACCAATTCACCAATTCGTCGAC 60
 Db 567 TTTAAGTCCCTAGCTCGATACCAATAAAGCCGCAATTCACCAATTCACCAATTCGTCGAC 626
 QY 61 CTC 63
 Db 627 CTC 629
 RESULT 35
 A48775
 LOCUS
 DEFINITION Sequence 2 from Patent WO9604388.
 ACCESSION A48775
 VERSION A48775.1 GI:2302445
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE
 1 (bases 1 to 6926)
 Browne, M.J., Murphy, K.E., Chapman, C.G., Clinkenbeard, H.E.,
 Young, P.R. and Shatzman, A.R.
 TITLE NOVEL COMPOUNDS
 JOURNAL Patent: WO 9604388-A 2 15-FEB-1996;

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COMMENT      SMITHKLINE BEECHAM PLC (GB)
FEATURES     Other publication AU 3382595 960304.
             Location/Qualifiers
             1..6926
             /organism="unidentified"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32644"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 6926;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAATAAGCCCAATTGACCAATTCACCACTTGGTGTGCAC 60
    |||||
Db 709 TTTAAGTCCTAGCTCGATACATAATAAGCCCAATTGACCAATTCACCACTTGGTGTGCAC 768

QY 61 CTC 63
    |||
Db 769 CTC 771

RESULT 36
AX743956/c
LOCUS      AX743956      6926 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5783181.
ACCESSION  AX743956
VERSION     AX743956.1 GI:3973817
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 6926)
AUTHORS     Browne,M.Joseph., Young,P.Ronald., Shatzman,A.Richard.,
             Murphy,K.Elizabeth, Chapman,C.Gerald. and
             Clinkenbeard,H.Elizabeth.
TITLE       Therapeutic uses of fusion proteins between mutant IL 4/IL13
JOURNAL     antagonists and immunoglobulins
PATENT      Patent: US 5783181-A 2 21-JUL-1998;
FEATURES     Location/Qualifiers
             1..6926
             /organism="unknown"
             /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 6926;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAATAAGCCCAATTGACCAATTCACCACTTGGTGTGCAC 60
    |||||
Db 709 TTTAAGTCCTAGCTCGATACATAATAAGCCCAATTGACCAATTCACCACTTGGTGTGCAC 768

QY 61 CTC 63
    |||
Db 769 CTC 771

RESULT 37
AX743955/c
LOCUS      AX743955      7086 bp      DNA      linear      PAT 14-MAY-2003
DEFINITION Sequence 3 from Patent WO0301630.
ACCESSION  AX743955
VERSION     AX743955.1 GI:30722652
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
             artificial sequences.
REFERENCE   1
AUTHORS     Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Orsini,G.
TITLE       Multi-cistronic vectors for gene transfer protocols
JOURNAL     Patent: WO 03031630-A 3 17-APR-2003;
             Keryos Spa (IT)

SMITHKLINE BEECHAM PLC (GB)
Other publication AU 3382595 960304.
Location/Qualifiers
1..7086
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 7086;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAATAAGCCCAATTGACCAATTCACCACTTGGTGTGCAC 60
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Db 1595 TTTAAGTCCTAGCTCGATACATAATAAGCCCAATTGACCAATTCACCACTTGGTGTGCAC 1536

QY 61 CTC 63
    |||
Db 1535 CTC 1533

RESULT 38
AX743956/c
LOCUS      AX743956      7334 bp      DNA      linear      PAT 14-MAY-2003
DEFINITION Sequence 4 from Patent WO0301630.
ACCESSION  AX743956
VERSION     AX743956.1 GI:30722653
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
             artificial sequences.
REFERENCE   1
AUTHORS     Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Orsini,G.
TITLE       Multi-cistronic vectors for gene transfer protocols
JOURNAL     Patent: WO 03031630-A 4 17-APR-2003;
             Keryos Spa (IT)

SMITHKLINE BEECHAM PLC (GB)
Other publication AU 3382595 960304.
Location/Qualifiers
1..7334
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 7334;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAATAAGCCCAATTGACCAATTCACCACTTGGTGTGCAC 60
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Db 1839 TTTAAGTCCTAGCTCGATACATAATAAGCCCAATTGACCAATTCACCACTTGGTGTGCAC 1780

QY 61 CTC 63
    |||
Db 1779 CTC 1777

RESULT 39
AR235458
LOCUS      AR235458      7492 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6461606.
ACCESSION  AR235458
VERSION     AR235458.1 GI:27278640
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 7492)
AUTHORS     Flotte,T.R., Sorg,S., Byrne,B.J. and Morgan,M.
TITLE       Materials and methods for gene therapy
JOURNAL     Patent: US 6461606-A 5 08-OCT-2002;
             Location/Qualifiers
             1..7492
             /organism="unknown"
             /mol_type="genomic DNA"

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ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 7492;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||||
 Db 27 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 86
 |||||

QY 61 CTC 63
 |||||
 Db 87 CTC 89

RESULT 40
 BD268239

LOCUS BD268239 8238 bp DNA linear PAT 17-JUL-2003

DEFINITION Adenovirus vector, packaging cell line, composition and method for production and use.

ACCESSION BD268239

VERSION BD268239.1 GI:33078007

KEYWORDS JP 2002534130-A/43.

SOURCE synthetic construct

ORGANISM artificial construct

REFERENCE 1 (bases 1 to 8238)
 Nemerow, G.R., Seggern, D.J.V., Hallenbeck, P.L., Stevenson, S.C. and Skripchenko, Y.

AUTHORS Skripchenko, Y.

TITLE Adenovirus vector, packaging cell line, composition and method for production and use

JOURNAL Patent: JP 2002534130-A 43 15-OCT-2002;
 NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE

COMMENT OS Artificial Sequence
 PN JP 2002534130-A/43
 PD 15-OCT-2002
 PF 14-JAN-2000 JP 2000593765
 PR 14-JAN-1999 US 60/115920
 PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO
 PC C12N15/09, A61K35/76, A61K48/00, A61P35/00, A61P43/00, A61P43/00, C12N5/10,
 PC C12N5/10, C12N15/00, C12N15/53, G01N33/566, C12N15/00, C12N5/00 CC
 Description of Artificial Sequence: plasmid

FT Key Location/Qualifiers
 FT source 1..8238
 /organism='Artificial Sequence'.

FEATURES

source
 1..8238
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8238;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||||
 Db 742 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 801
 |||||

QY 61 CTC 63
 |||||
 Db 802 CTC 804

RESULT 41
 XXU02432

LOCUS XXU02432 8413 bp DNA circular SYN 29-JAN-1997

DEFINITION Cloning vector pMAMneo, complete sequence.

ACCESSION U02432

VERSION U02432.1 GI:413798

KEYWORDS

SOURCE Cloning vector pMAMneo
 ORGANISM Cloning vector pMAMneo
 REFERENCE 1 (bases 1 to 8413)
 AUTHORS Kitts, P.A.
 JOURNAL CLONTECH Vectors On Disc version 1.3
 REFERENCE 2 (bases 1 to 8413)
 AUTHORS Kitts, P.A.
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA

COMMENT

This vector can be obtained from CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, please contact your local distributor. For technical information, call (415) 424-8222 or (800) 662-2566, extension 3. This sequence has been compiled from information in the sequence databases, published literature and other sources, together with partial sequences obtained by CLONTECH; this vector has not been completely sequenced. If you suspect there is an error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.

FEATURES

Location/Qualifiers

source
 1..8413
 /organism="Cloning vector pMAMneo"
 /mol_type="genomic DNA"
 /db_xref="taxon:31818"

ORIGIN

Query Match 100.0%; Score 63; DB 12; Length 8413;
 Best Local Similarity 100.0%; Pred. No. 1.6e-13;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||||
 Db 27 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 86
 |||||

QY 61 CTC 63
 |||||
 Db 87 CTC 89

RESULT 42

XXU02430

LOCUS XXU02430 8475 bp DNA circular SYN 29-JAN-1997

DEFINITION Cloning vector pMAMneoBlue, complete sequence.

ACCESSION U02430

VERSION U02430.1 GI:413796

KEYWORDS

SOURCE Cloning vector pMAMneoBlue
 ORGANISM Cloning vector pMAMneoBlue
 REFERENCE 1 (bases 1 to 8475)
 AUTHORS Kitts, P.A.

TITLE

CLONTECH Vectors On Disc version 1.3

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 8475)

AUTHORS

Kitts, P.A.

TITLE

Direct Submission

JOURNAL

Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA

COMMENT

This sequence has been compiled from information in the sequence databases, published literature and other sources, together with partial sequences obtained by CLONTECH. This vector is no longer available from CLONTECH and CLONTECH will not update or revise this sequence.

FEATURES

Location/Qualifiers

source
 1..8475
 /organism="Cloning vector pMAMneoBlue"
 /mol_type="genomic DNA"

/db_xref="taxon:31821"

ORIGIN

Query Match 100.0%; Score 63; DB 12; Length 8475;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 60
|||||
Db 27 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 86
|||||

QY 61 CTC 63
|||
Db 87 CTC 89

RESULT 43

LOCUS 158322 I58322 8591 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5652092.
ACCESSION I58322
VERSION I58322.1 GI:2477560
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL Patent: US 5652092-A 6 29-JUL-1997;
FEATURES Location/Qualifiers
source 1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 60
|||||
Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 5236
|||||

QY 61 CTC 63
|||
Db 5237 CTC 5239

RESULT 44

LOCUS 158323 I58323 8591 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 8 from patent US 5652092.
ACCESSION I58323
VERSION I58323.1 GI:2477561
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL Patent: US 5652092-A 8 29-JUL-1997;
FEATURES Location/Qualifiers
source 1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 60
|||||
Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 5236
|||||

QY 61 CTC 63
|||
Db 5237 CTC 5239

RESULT 45

LOCUS 160508 I60508 8591 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 6 from patent US 5656477.
ACCESSION I60508
VERSION I60508.1 GI:2478953
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL Patent: US 5656477-A 6 12-AUG-1997;
FEATURES Location/Qualifiers
source 1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 60
|||||
Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 5236
|||||

QY 61 CTC 63
|||
Db 5237 CTC 5239

RESULT 46

LOCUS 160509 I60509 8591 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 8 from patent US 5656477.
ACCESSION I60509
VERSION I60509.1 GI:2478954
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek,M.Peter. and Jacobsen,J.Steven.
TITLE Amyloid precursor proteins and method of using same to assess agents which down-regulate formation of .beta.-amyloid peptide
JOURNAL Patent: US 5656477-A 8 12-AUG-1997;
FEATURES Location/Qualifiers
source 1..8591
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 60
|||||
Db 5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGGACCAATTCACCACATTGGTGTGCAC 5236
|||||


```

QY      61 CTC 63
Db      5237 CTC 5239

RESULT 47
LOCUS   177052
DEFINITION Sequence 6 from patent US 5693478.
ACCESSION 177052
VERSION 177052.1 GI:3013206
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.
TITLE Method of detecting amyloid precursor proteins
JOURNAL Patent: US 5693478-A 6 02-DEC-1997;
FEATURES Location/Qualifiers
          source
            1..8591
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db      5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60

QY      61 CTC 63
Db      5237 CTC 5239

RESULT 48
LOCUS   177053
DEFINITION Sequence 8 from patent US 5693478.
ACCESSION 177053
VERSION 177053.1 GI:3013207
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.
TITLE Method of detecting amyloid precursor proteins
JOURNAL Patent: US 5693478-A 8 02-DEC-1997;
FEATURES Location/Qualifiers
          source
            1..8591
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db      5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60

QY      61 CTC 63
Db      5237 CTC 5239

RESULT 49
LOCUS   XXU02431
DEFINITION Cloning vector pMAMneo-CAT, complete sequence.
ACCESSION U02431
VERSION U02431.1 GI:413797

```

```

187173
LOCUS   187173
DEFINITION Sequence 6 from patent US 5703209.
ACCESSION 187173
VERSION 187173.1 GI:3206891
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.
TITLE Amyloid precursor proteins and method of using same to assess
JOURNAL Patent: US 5703209-A 6 30-DEC-1997;
FEATURES Location/Qualifiers
          source
            1..8591
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db      5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60

QY      61 CTC 63
Db      5237 CTC 5239

RESULT 50
LOCUS   187174
DEFINITION Sequence 8 from patent US 5703209.
ACCESSION 187174
VERSION 187174.1 GI:3206892
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 8591)
AUTHORS Vitek, M. Peter, and Jacobsen, J. Steven.
TITLE Amyloid precursor proteins and method of using same to assess
JOURNAL Patent: US 5703209-A 8 30-DEC-1997;
FEATURES Location/Qualifiers
          source
            1..8591
              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 63; DB 6; Length 8591;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60
Db      5177 TTTAAGTGCCTAGCTCGATACATAAAGCGCAATTGACCAATTCACCAATTTGGTGTGCAC 60

QY      61 CTC 63
Db      5237 CTC 5239

RESULT 51
LOCUS   XXU02431
DEFINITION Cloning vector pMAMneo-CAT, complete sequence.
ACCESSION U02431
VERSION U02431.1 GI:413797

```

KEYWORDS
SOURCE Cloning vector pMAMneo-CAT
ORGANISM Cloning vector pMAMneo-CAT
artificial sequences; vectors.
REFERENCE
AUTHORS 1 (bases 1 to 9184)
TITLE ClONTECH Vectors On Disc version 1.3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9184)
AUTHORS Kitts,P.A.
JOURNAL Direct Submission
TITLE Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020
JOURNAL 1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT This vector can be obtained from CLONTECH Laboratories, Inc. To place an order
East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
call (415) 424-8222 or (800) 662-2566, extension 1. International
customers, please contact your local distributor. For technical
information, call (415) 424- 8222 or (800) 662-2566, extension 3.
This sequence has been compiled from information in the sequence
databases, published literature and other sources, together with
partial sequences obtained by CLONTECH; this vector has not been
completely sequenced. If you suspect there is an error in this
sequence, please contact CLONTECH's Technical Service Department at
(415) 424-8222 or (800) 662-2566, extension 3 or E-mail
TECH@CLONTECH.COM.

FEATURES
source
1..9184
Location/Qualifiers
/organism="Cloning vector pMAMneo-CAT"
/mol_type="genomic DNA"
/db_xref="taxon:31819"

ORIGIN
Query Match 100.0%; Score 63; DB 12; Length 9184;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACAAATAAAGCGCATTGGACCATTCACCACATTGGTGTGCAC 60
|||||
Db 27 TTTAAGTGCCTAGCTCGATACAAATAAAGCGCATTGGACCATTCACCACATTGGTGTGCAC 86
|||||

QY 61 CTC 63
|||
Db 87 CTC 89
|||

RESULT 52
AR215118 9737 bp DNA linear PAT 25-SEP-2002
LOCUS
DEFINITION Sequence 22 from patent US 6410266.
ACCESSION AR215118
VERSION AR215118.1 GI:23313246
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6410266-A 22 25-JUN-2002;
FEATURES
source
1..9737
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 9737;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACAAATAAAGCGCATTGGACCATTCACCACATTGGTGTGCAC 60
|||||
Db 1613 TTTAAGTGCCTAGCTCGATACAAATAAAGCGCATTGGACCATTCACCACATTGGTGTGCAC 1672
|||||

QY 61 CTC 63
|||
Db 1673 CTC 1675
|||

RESULT 53
AR215119 9737 bp DNA linear PAT 25-SEP-2002
LOCUS
DEFINITION Sequence 23 from patent US 6410266.
ACCESSION AR215119
VERSION AR215119.1 GI:23313247
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6410266-A 23 25-JUN-2002;
FEATURES
source
1..9737
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 63; DB 6; Length 9737;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACAAATAAAGCGCATTGGACCATTCACCACATTGGTGTGCAC 60
|||||
Db 1613 TTTAAGTGCCTAGCTCGATACAAATAAAGCGCATTGGACCATTCACCACATTGGTGTGCAC 1672
|||||

QY 61 CTC 63
|||
Db 1673 CTC 1675
|||

RESULT 54
AR215124 9737 bp DNA linear PAT 25-SEP-2002
LOCUS
DEFINITION Sequence 28 from patent US 6410266.
ACCESSION AR215124
VERSION AR215124.1 GI:23313252
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6410266-A 28 25-JUN-2002;
FEATURES
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/organism="unknown"
/mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1613 TTTAAGTGCCTAGCTCGATACAAATAAAGCGCATTGGACCATTCACCACATTGGTGTGCAC 1672
|||||

QY 61 CTC 63
|||
Db 1673 CTC 1675
|||

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RESULT 55
AR302360
LOCUS AR302360 9737 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 22 from patent US 6541221.
ACCESSION AR302360
VERSION AR302360.1 GI:31690614
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 9737)
Harrington,J.J., Sherf,B. and Rundlett,S.
AUTHORS
TITLE Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6541221-A 22 01-APR-2003;
FEATURES
source
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/mol_type="genomic DNA"
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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1613 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCACTTGGTGTGCAC 1672
QY 61 CTC 63
Db 1673 CTC 1675
RESULT 56
AR302361
LOCUS AR302361 9737 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 23 from patent US 6541221.
ACCESSION AR302361
VERSION AR302361.1 GI:31690615
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 9737)
Harrington,J.J., Sherf,B. and Rundlett,S.
AUTHORS
TITLE Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6541221-A 23 01-APR-2003;
FEATURES
source
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QY 61 CTC 63
Db 1673 CTC 1675
RESULT 57
AR302366
LOCUS AR302366 9737 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 28 from patent US 6541221.
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ACCESSION AR302366
VERSION AR302366.1 GI:31690620
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 9737)
Harrington,J.J., Sherf,B. and Rundlett,S.
AUTHORS
TITLE Compositions and methods for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6541221-A 28 01-APR-2003;
FEATURES
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QY 61 CTC 63
Db 1673 CTC 1675
RESULT 58
AR373232
LOCUS AR373232 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 22 from patent US 6602686.
ACCESSION AR373232
VERSION AR373232.1 GI:40075240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 9737)
Harrington,J.J., Sherf,B. and Rundlett,S.
AUTHORS
TITLE Compositions and method for non-targeted activation of endogenous
genes
JOURNAL Patent: US 6602686-A 22 05-AUG-2003;
FEATURES
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QY 61 CTC 63
Db 1673 CTC 1675
RESULT 59
AR373233
LOCUS AR373233 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6602686.
ACCESSION AR373233
VERSION AR373233.1 GI:40075241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 23 05-AUG-2003;
FEATURES Location/Qualifiers
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QY 61 CTC 63
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Db 1673 CTC 1675

RESULT 60
AR373238
LOCUS AR373238 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 28 from patent US 6602686.
ACCESSION AR373238
VERSION AR373238.1 GI:40075246
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 28 05-AUG-2003;
FEATURES Location/Qualifiers
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QY 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 61
AR401618
LOCUS AR401618 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 22 from patent US 6623958.
ACCESSION AR401618
VERSION AR401618.1 GI:40149066
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes

JOURNAL Patent: US 6623958-A 22 23-SEP-2003;
FEATURES Location/Qualifiers
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Db 1613 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCAATTCACCACATTGGTGTGCAC 1672

QY 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 62
AR401619
LOCUS AR401619 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 23 from patent US 6623958.
ACCESSION AR401619
VERSION AR401619.1 GI:40149067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 23 23-SEP-2003;
FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1613 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCAATTCACCACATTGGTGTGCAC 1672

QY 61 CTC 63
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Db 1673 CTC 1675

RESULT 63
AR401624
LOCUS AR401624 9737 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 28 from patent US 6623958.
ACCESSION AR401624
VERSION AR401624.1 GI:40149072
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9737)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 28 23-SEP-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

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Db 1807 CTC 1809

RESULT 68
LOCUS AR215121 10060 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 25 from patent US 6410266.
ACCESSION AR215121
VERSION AR215121.1 GI:23313249
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10060)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6410266-A 25 25-JUN-2002;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

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Qy 61 CTC 63
Db 1996 CTC 1998

RESULT 69
LOCUS AR302363 10060 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 25 from patent US 6541221.
ACCESSION AR302363
VERSION AR302363.1 GI:31690617
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10060)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6541221-A 25 01-APR-2003;
FEATURES Location/Qualifiers
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Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 1936 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1995

Qy 61 CTC 63
Db 1996 CTC 1998

RESULT 70
LOCUS AR373235 10060 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 25 from patent US 6602686.
ACCESSION AR373235
VERSION AR373235.1 GI:40075243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10060)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and method for non-targeted activation of endogenous genes
JOURNAL Patent: US 6602686-A 25 05-AUG-2003;
FEATURES Location/Qualifiers
source 1..10060
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Qy 61 CTC 63
Db 1996 CTC 1998

RESULT 71
LOCUS AR401621 10060 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 25 from patent US 6623958.
ACCESSION AR401621
VERSION AR401621.1 GI:40149069
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10060)
AUTHORS Harrington,J.J., Sherf,B. and Rundlett,S.
TITLE Compositions and methods for non-targeted activation of endogenous genes
JOURNAL Patent: US 6623958-A 25 23-SEP-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 1.6e-13;
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Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 1936 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1995

Qy 61 CTC 63
Db 1996 CTC 1998

RESULT 72
LOCUS U02448 10339 bp DNA circular SYN 29-MAR-1996
DEFINITION Cloning vector pMAMneo-LUC, complete sequence.
ACCESSION U02448

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VERSION      U02448.1  GI:413814
KEYWORDS     Cloning vector pMAmneo-LUC
SOURCE       Cloning vector pMAmneo-LUC
ORGANISM     artificial sequences; vectors.
REFERENCE    1 (bases 1 to 10339)
AUTHORS      Kitts,P.A.
JOURNAL      CLONTECH Vectors On Disc version 1.3
TITLE        Unpublished
REFERENCE    2 (bases 1 to 10339)
AUTHORS      Kitts,P.A.
JOURNAL      Direct Submission
TITLE        Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
JOURNAL      1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT      In reference 2, this vector is referred to as pBSpac delta P. This
              vector can be obtained from CLONTECH Laboratories, Inc., 1020 East
              Meadow Circle, Palo Alto, CA 94303, USA. To place an order call
              (415) 424-8222 or (800) 662-2566, extension 1. International
              customers, please contact your local distributor. For technical
              information, call (415) 424- 8222 or (800) 662-2566, extension 3.
              This sequence was compiled by Susana de la Luna. If you suspect
              there is an error in this sequence, please contact CLONTECH's
              Technical Service Department at (415) 424-8222 or (800) 662-2566,
              extension 3 or E-mail TECH@CLONTECH.COM.

FEATURES     source
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              /organism="Cloning vector pMAmneo-LUC"
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QY  1  TTTAAGTCCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTTGGTGTGCAC 60
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QY   61  CTC 63
Db    87  CTC 89

RESULT 73
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LOCUS        XXU02428      10377 bp      DNA      circular SYN 29-JAN-1997
DEFINITION   Cloning vector pDR2, complete sequence.
ACCESSION    U02428
VERSION      U02428.1  GI:413794
KEYWORDS     Cloning vector pDR2
SOURCE       Cloning vector pDR2
ORGANISM     artificial sequences; vectors.
REFERENCE    1 (bases 1 to 10377)
AUTHORS      Murphy,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.
TITLE        cDNA expression cloning in human cells using the p.lambdadr2
JOURNAL      episomal vector system
REFERENCE    2 (bases 1 to 10377)
AUTHORS      Kitts,P.A.
JOURNAL      CLONTECH Vectors On Disc version 1.3
TITLE        Unpublished
REFERENCE    3 (bases 1 to 10377)
AUTHORS      Kitts,P.A.
JOURNAL      Direct Submission
TITLE        Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
JOURNAL      1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT      This vector can be obtained from CLONTECH Laboratories, Inc., 1020
              East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
              call (415) 424-8222 or (800) 662-2566, extension 1. International
              customers, please contact your local distributor. For technical
              information, call (415) 424- 8222 or (800) 662-2566, extension 3.

This sequence has been compiled from information in the sequence
databases, published literature and other sources, together with
partial sequences obtained by CLONTECH; this vector has not been
completely sequenced. If you suspect there is an error in this
sequence, please contact CLONTECH's Technical Service Department at
(415) 424-8222 or (800) 662-2566, extension 3 or E-mail
TECH@CLONTECH.COM.

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QY   61  CTC 63
Db    669  CTC 671

RESULT 74
U02455
LOCUS        U02455      10850 bp      DNA      circular SYN 29-MAR-1996
DEFINITION   Cloning vector rpDR2, complete sequence.
ACCESSION    U02455
VERSION      U02455.1  GI:413821
KEYWORDS     Cloning vector rpDR2
SOURCE       Cloning vector rpDR2
ORGANISM     artificial sequences; vectors.
REFERENCE    1 (bases 1 to 10850)
AUTHORS      Kitts,P.A.
JOURNAL      CLONTECH Vectors On Disc version 1.3
TITLE        Unpublished
REFERENCE    2 (bases 1 to 10850)
AUTHORS      Murphy,A.J., Kung,A.L., Swirski,R.A. and Schimke,R.T.
TITLE        cDNA expression cloning in human cells using the p.lambdadr2
JOURNAL      episomal vector system
REFERENCE    3 (bases 1 to 10850)
AUTHORS      Kitts,P.A.
JOURNAL      Direct Submission
TITLE        Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
JOURNAL      1020 East Meadow Circle, Palo Alto, CA 94303, USA
COMMENT      Lambda DR2 can be obtained from CLONTECH Laboratories, Inc., 1020
              East Meadow Circle, Palo Alto, CA 94303, USA. To place an order
              call (415) 424-8222 or (800) 662-2566, extension 1. International
              customers, please contact your local distributor. For technical
              information, call (415) 424- 8222 or (800) 662-2566, extension 3.
              This sequence was compiled by Andrew Murphy and revised at
              CLONTECH. If you suspect there is an error in this sequence, please
              contact CLONTECH's Technical Service Department at (415) 424-8222
              or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.

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Db 609 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 668
QY 61 CTC 63
Db 669 CTC 671

RESULT 75
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LOCUS Sequence 1 from Patent WO9844129.
DEFINITION AX031159
ACCESSION AX031159
VERSION AX031159.1 GI:10278512
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Lew, A.M., Boyle, J.S. and Brady, J.L.
TITLE Enhancement of immune response using targeting molecules
JOURNAL Patent: WO 9844129-A 1 08-OCT-1998;
INST MEDICAL W & E HALL (AU); QUEENSLAND INST MED RES (AU); CSL
LTD (AU); LEW ANDREW MARK (AU); UNIV MELBOURNE (AU); BOYLE
JEFFREY STEPHEN (AU); BRADY JAMIE LOUISE (AU); COMMW SCIENT IND
RES ORG (AU)

FEATURES
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QY 61 CTC 63
Db 631 CTC 633

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Job time : 355.355 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 03:02:06 ; Search time 54.4024 Seconds
(without alignments)
4919.575 Million cell updates/sec

Title: US-09-733-368a-1_COPY_550_612
Perfect score: 63
Sequence: 1 tttaagcgctagctcgata.....accacattggtgcacctc 63

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	63	100.0	397	3	Aaz94161 395 Nucle
3	63	100.0	397	3	Aa14719 Nucleotid
4	63	100.0	397	3	Aaz93077 Rous sarc
5	63	100.0	648	4	Aa43951 Rous sarc
6	63	100.0	2187	3	Aa14722 Nucleotid
7	63	100.0	2829	3	Aaz93333 Partial s
8	63	100.0	2878	3	Aaz93078 Partial s
9	63	100.0	3188	2	Aa06310 Sequence
10	63	100.0	3276	2	Aa06311 Sequence
11	63	100.0	3310	3	Aaz93331 Partial s
12	63	100.0	3311	3	Aaz93079 Partial s
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14	63	100.0	3427	2	Aa06310 Sequence
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16	63	100.0	4059	2	Aa06312 Sequence
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18	63	100.0	4341	2	Aa06312 Sequence
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20	63	100.0	4341	2	Aa06312 Sequence
21	63	100.0	4457	9	Abn83143 Plasmid p
22	63	100.0	4487	3	Abn83143 Plasmid p
23	63	100.0	5653	2	Aa09085 AGRSV-bet
					Aa02998 RSV tar R

ALIGNMENTS

KW replication-deficient adenovirus type 5; suicide gene therapy;
 KW cancer cell; chemotherapy; beta-lactamase prodnrg enzyme; prodrg TCM;
 KW anticancer; tumor; leukemia; breast cancer; Wilm's tumor;
 KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;
 KW papillary adenocarcinoma; promoter; ss.
 XX
 OS Rous sarcoma virus.
 XX
 XX WO2000020608-A1.
 XX PN

PD 13-APR-2000.
 XX
 PF 01-OCT-1999; 99WO-US020908.
 XX
 PR 02-OCT-1998; 98US-00165321.
 XX
 PA (GENO-) GENOTHERAPEUTICS INC.
 XX
 PI Steiner MS;
 XX
 DR WPI; 2000-303788/26.
 XX
 PT Treating cancer using viral vectors which encode enzymes that convert
 PT inactive drugs to active cytotoxic agents, expression of the enzyme is
 PT tissue specific therefore targeting the effects of the drug to tumor
 PT cells.
 XX
 PS Disclosure; Page 13-14; 130pp; English.
 XX
 CC The specification describes a method for inducing cellular cytotoxicity
 CC in tumor cells using replication-deficient adenovirus type 5 expression
 CC vectors. The vectors comprise a sequence encoding a beta-lactamase under
 CC the control of a Rous Sarcoma virus in combination with a prodrug
 CC conjugated to a toxic agent. Tissue specific expression of the enzyme
 CC converts the inactive drugs into active cancer killing agents. The
 CC adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-
 CC lactamase sequence is inserted within this region. The vectors are used
 CC for suicide gene therapy. This involves introducing genes into cancer
 CC cells that encode enzymes capable of converting inactive drugs into
 CC active cancer killing agents. If tissue specific promoters are coupled to
 CC the prodrug enzymes, then production of the prodrug will be tissue
 CC specific and targeted to the tumor. Therefore the cancer cells act as
 CC their own factories to activate chemotherapy agents and commit suicide.
 CC Beta-lactamase prodrug enzymes convert prodrug TCM into an active
 CC anticancer agent which is cytotoxic to cancer cells PPC-1. The method is
 CC used to treat patients with cancers of the brain, bladder or prostate. It
 CC may also be used to treat a range of other tumors such as leukemia,
 CC breast cancer, Wilms' tumor, small cell lung carcinoma, Ewing's sarcoma,
 CC colon carcinoma and papillary adenocarcinomas. The present sequence
 CC represents the Rous Sarcoma virus promoter, which was used to
 CC construct vectors of the invention
 XX
 SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 397;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 DB 334 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 393
 QY 61 CTC 63
 DB 394 CTC 396

RESULT 4
 AAH43951
 ID AAH43951 standard; DNA; 397 BP.
 XX
 AC AAH43951;
 XX
 DT 04-JUL-2000 (first entry)
 XX
 DE Rous Sarcoma Virus promoter sequence.
 XX
 KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
 KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 XX
 OS Rous sarcoma virus.
 XX
 PN WO200142444-A2.
 XX
 PD 14-JUN-2001.

PN WO20014256-A1.
 XX
 PD 16-MAR-2000.
 XX
 PF 03-SEP-1999; 99WO-US018834.
 XX
 PR 04-SEP-1998; 98US-00148275.
 XX
 PA (GENO-) GENOTHERAPEUTICS INC.
 XX
 PI Steiner MS, Lu Y;
 XX
 DR WPI; 2000-257001/22.
 XX
 PT Replication-deficient adenovirus type 5 expression vectors used for gene
 PT therapy of cancer, especially prostate cancer, comprising an insertion of
 PT nucleic acid encoding cytochrome p450 genes.
 XX
 PS Claim 8; Page 18; 110pp; English.
 XX
 CC Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (III) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene
 XX
 SQ Sequence 397 BP; 108 A; 79 C; 110 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 397;
 Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 DB 334 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 393
 QY 61 CTC 63
 DB 394 CTC 396

RESULT 5
 AAH43951
 ID AAH43951 standard; DNA; 648 BP.
 XX
 AC AAH43951;
 XX
 DT 06-SEP-2001 (first entry)
 XX
 DE Rous sarcoma virus promoter nucleotide sequence SEQ ID NO:1.
 XX
 KW Rous sarcoma virus; promoter; enhancer; RSV; primate; gene expression;
 KW transgene; genetic engineering; gene therapy; immunisation; ds.
 XX
 OS Rous sarcoma virus.
 XX
 PN WO200142444-A2.
 XX
 PD 14-JUN-2001.

XX 08-DEC-2000; 2000WO-US033256.
 XX
 XX
 XX 10-DEC-1999; 99US-0170019P.
 XX
 XX (ARIA-) ARIAD GENE THERAPEUTICS INC.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX
 XX Rivera V, Zoltick P, Wilson JM;
 XX WPI; 2001-381673/40.
 XX
 XX Genetically engineering a primate for expression of a desired gene,
 XX comprises introducing into the primate a transgene comprising Rous
 XX Sarcoma Virus (RSV) promoter and a nucleic acid sequence heterologous to
 XX RSV promoter.
 XX
 XX Claim 7; Page 44; 64pp; English.
 XX
 XX The present invention describes a method for genetically engineering a
 XX primate for expression of a desired gene comprising introducing into the
 XX primate a transgene comprising an Rous Sarcoma Virus (RSV) promoter and a
 XX nucleic acid sequence heterologous to RSV promoter. Also described is a
 XX primate cell (I) containing and capable of expressing a transgene
 XX comprising an RSV promoter operably linked to a recombinant nucleic acid
 XX encoding one or more fusion proteins, where the fusion proteins bind to a
 XX ligand and in the presence of the ligand modulate(s) the expression level
 XX of a target gene. The method can be used for high level expression of
 XX genes in primates or for engineering primate cells. It is useful for
 XX increasing the efficacy of many gene therapy strategies, and for
 XX increasing the efficacy of intracellular immunisation agents, molecules
 XX like ribozymes, antisense RNA, and dominant negative proteins, that act
 XX either stoichiometrically, or by competition. The method increases the
 XX efficacy of many gene therapy strategies by substantially elevating the
 XX expression of an exogenous therapeutic gene, and allowing expression to
 XX reach therapeutically effective levels. The present sequence represents a
 XX specifically claimed RSV enhancer/promoter nucleotide sequence from the
 XX present invention
 XX
 XX Sequence 648 BP; 163 A; 135 C; 179 G; 171 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 63; DB 4; Length 648;
 XX Best Local Similarity 100.0%; Pred. No. 2.2e-14;
 XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 TTTAAGTGGCTAGCTCGATACATTAAGCCGATTGGACCATTCACCATTTGGTGGAC 60
 XX 550 TTTAAGTGGCTAGCTCGATACATTAAGCCGATTGGACCATTCACCATTTGGTGGAC 609
 XX
 XX QY 61 CTC 63
 XX 610 CTC 612
 XX
 XX Db
 XX
 XX RESULT 6
 XX AA14722
 XX ID AA14722 standard; DNA; 2187 BP.
 XX
 XX AC AA14722;
 XX
 XX DT 06-AUG-2003 (revised)
 XX DT 08-AUG-2000 (first entry)
 XX
 XX DE Nucleotide sequence of region A of vector Ad5RSVbeta-lactamase.
 XX
 XX KW Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase;
 XX KW replication-deficient adenovirus type 5; suicide gene therapy;
 XX KW cancer cell; chemotherapy; beta-lactamase prodrug enzyme; prodrug TCM;
 XX KW anticancer; tumor; leukemia; breast cancer; Wilms' tumor;
 XX KW small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;
 XX KW papillary adenocarcinoma; ss.
 XX
 XX XX Synthetic.

OS Rous sarcoma virus.
 OS Mastadenovirus.
 XX WO2000020608-A1.
 XX 13-APR-2000.
 XX
 XX 01-OCT-1999; 99WO-US020908.
 XX
 XX 02-OCT-1998; 98US-00165321.
 XX (GENO-) GENOTHERAPEUTICS INC.
 XX Steiner MS;
 XX WPI; 2000-303788/26.
 XX
 XX Treating cancer using viral vectors which encode enzymes that convert
 XX inactive drugs to active cytotoxic agents, expression of the enzyme is
 XX tissue specific therefore targeting the effects of the drug to tumor
 XX cells.
 XX
 XX Disclosure; Fig 10; 130pp; English.
 XX
 XX The specification describes a method for inducing cellular cytotoxicity
 XX in tumor cells using replication-deficient adenovirus type 5 expression
 XX vectors. The vectors comprise a sequence encoding a beta-lactamase under
 XX the control of a Rous Sarcoma virus in combination with a prodrug
 XX conjugated to the toxic agent. Tissue specific expression of the enzyme
 XX converts the inactive drugs into active cancer killing agents. The
 XX adenovirus genome has a deletion in an E1 and/or E3 region, and the beta-
 XX lactamase sequence is inserted within this region. The vectors are used
 XX for suicide gene therapy. This involves introducing genes into cancer
 XX cells that encode enzymes capable of converting inactive drugs into
 XX active cancer killing agents. If tissue specific promoters are coupled to
 XX the prodrug enzymes, then production of the prodrug will be tissue
 XX specific and targeted to the tumor. Therefore the cancer cells act as
 XX their own factories to activate chemotherapy agents and commit suicide.
 XX Beta-lactamase prodrug enzymes convert prodrug TCM into an active
 XX anticancer agent which is cytotoxic to cancer cells PPC-1. The method is
 XX used to treat patients with cancers of the brain, bladder or prostate. It
 XX may also be used to treat a range of other tumors such as leukemia,
 XX breast cancer, Wilms' tumor, small cell lung carcinoma, Ewing's sarcoma,
 XX colon carcinoma and papillary adenocarcinomas. The present sequence
 XX represents region A of vector Ad5RSVbeta-lactamase, a vector of the
 XX invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX
 XX Sequence 2187 BP; 562 A; 477 C; 592 G; 556 T; 0 U; 0 Other;
 XX
 XX Query Match 100.0%; Score 63; DB 3; Length 2187;
 XX Best Local Similarity 100.0%; Pred. No. 2.9e-14;
 XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 TTTAAGTGGCTAGCTCGATACATTAAGCCGATTGGACCATTCACCATTTGGTGGAC 60
 XX 742 TTTAAGTGGCTAGCTCGATACATTAAGCCGATTGGACCATTCACCATTTGGTGGAC 801
 XX
 XX QY 61 CTC 63
 XX 802 CTC 804
 XX
 XX Db
 XX
 XX RESULT 7
 XX AA293333
 XX ID AA293333 standard; DNA; 2829 BP.
 XX
 XX AC AA293333;
 XX
 XX DT 04-JUL-2000 (first entry)
 XX
 XX DE Partial sequence of replication deficient adenoviral vector Ad5RSV2C9.
 XX
 XX KW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;

KW Rous Sarcoma virus; BSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 XX Synthetic.
 OS
 XX WO200014256-A1.
 XX
 XX 16-MAR-2000.
 XX
 XX 03-SEP-1999; 99WO-US018834.
 XX
 XX 04-SEP-1998; 98US-00148275.
 XX
 XX (GENO-) GENOTHERAPEUTICS INC.
 XX
 XX Steiner MS, Lu Y;
 XX
 XX WPI; 2000-257001/22.
 XX
 XX Replication-deficient adenovirus type 5 expression vectors used for gene
 PT therapy of cancer, especially prostate cancer, comprising an insertion of
 PT nucleic acid encoding cytochrome p450 genes.
 XX
 XX Claim 16; Fig 11A; 110pp; English.

XX Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: Vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated AdRSV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated AdRSV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated AdRSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (III) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitise the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene. This sequence is
 CC designated region A of the vector AdRSV2C9 and is the sequence of the
 CC cytochrome 2C9 p450
 XX
 XX Sequence 2829 BP; 748 A; 633 C; 707 G; 741 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 2829;
 Best Local Similarity 100.0%; Pred. No. 3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
 Db 742 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 801
 QY 61 CTC 63
 Db 802 CTC 804

RESULT 8
 AAZ93078
 ID AAZ93078 standard; DNA; 2878 BP.
 XX
 XX AAZ93078;
 XX
 XX 04-JUL-2000 (first entry)
 DT
 XX Partial sequence of replication deficient adenoviral vector AdRSV3A4.
 DE
 XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;
 KW

KW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;
 KW prodrug; nicotinamide adenine dinucleotide phosphatase; ss.
 XX Synthetic.
 OS
 XX WO200014256-A1.
 XX
 XX 16-MAR-2000.
 XX
 XX 03-SEP-1999; 99WO-US018834.
 XX
 XX 04-SEP-1998; 98US-00148275.
 XX
 XX (GENO-) GENOTHERAPEUTICS INC.
 XX
 XX Steiner MS, Lu Y;
 XX
 XX WPI; 2000-257001/22.
 XX
 XX Replication-deficient adenovirus type 5 expression vectors used for gene
 PT therapy of cancer, especially prostate cancer, comprising an insertion of
 PT nucleic acid encoding cytochrome p450 genes.
 XX
 XX Claim 17; Fig 11B; 110pp; English.

XX Replication-deficient adenovirus type 5 expression vectors comprise an
 CC adenovirus genome with a deletion in the E1 and E2 region of the genome
 CC and an insertion within the region under the control of a Rous Sarcoma
 CC virus promoter can be used to induce chemotoxicity in tumour cells. Three
 CC such expression vectors are described, the inserted nucleic acids in each
 CC being the following: Vector (I) has an insertion of a nucleic acid
 CC encoding a cytochrome 2C9 p450 and is designated AdRSV2C9 (ATCC VR-
 CC 2628). Vector (II) has an insertion of a nucleic acid encoding a
 CC cytochrome 3A4 p450 and is designated AdRSV3A4 (ATCC VR-2629). Vector
 CC (III) has an insertion of a nucleic acid encoding a nicotinamide adenine
 CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is
 CC designated AdRSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell
 CC can be induced by administering (I) and (III) or (II) and (III) into the
 CC tumor cell (e.g. a prostate tumor cell) to selectively sensitise the cell
 CC to a prodrug and then administering the prodrug which kills the cell,
 CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug
 CC therapy to transfer a drug susceptibility gene to the tumor which
 CC activates a nontoxic prodrug intratumorally so the released drug can kill
 CC the tumor cells containing the drug susceptibility gene. This sequence is
 CC designated region A of the vector AdRSV3A4 and is the sequence of the
 CC cytochrome 3A4 p450
 XX
 XX Sequence 2878 BP; 786 A; 609 C; 710 G; 773 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 2878;
 Best Local Similarity 100.0%; Pred. No. 3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
 Db 742 TTTAAGTGCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 801
 QY 61 CTC 63
 Db 802 CTC 804

RESULT 9
 AAQ06310
 ID AAQ06310 standard; DNA; 3188 BP.
 XX
 XX AAQ06310;
 XX
 XX 25-MAR-2003 (revised)
 DT
 XX 29-JAN-1991 (first entry)
 DE
 XX Sequence of plasmid p79DBAM.
 XX

XW IFN-gamma receptor; autoimmune disease; multiple sclerosis;
XX hypersensitivity; ds.
OS Homo sapiens.

XX

PH Key Location/Qualifiers

XX LTR

XX 279..335

XX /*tag= a

XX polyA_signal

XX 497..502

XX /*tag= b

XX PN EP393502-A.

XX PD 24-OCT-1990.

XX PF 11-APR-1990; 90EP-00106992.

XX PR 19-APR-1989; 89EP-00810295.

XX PA (HOFF) HOFFMANN-LA ROCHE AG.

XX PI Fountoulak M, Garotta G, Stuber D;

XX WPI; 1990-322042/43.

XX DR Soluble interferon-gamma receptors - for treating auto-immune diseases,
XX PT chronic inflammations, etc.

XX PS Disclosure; Fig 49; 174pp; English.

XX CC IFN-gamma is a therapeutically active agent in the treatment of
XX auto-immune disease, allograft transplant rejections, multiple sclerosis,
XX chronic inflammations and delayed hypersensitivity. It is also useful in
XX identifying IFN-gamma agonists and antagonists. See also AAQ06301.
XX (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 3188 BP; 797 A; 774 C; 882 G; 735 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 63; DB 2; Length 3188;

XX Best Local Similarity 100.0%; Pred. No. 3.1e-14;

XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTCGGTGTGCAC 60

Db 250 TTTAAGTCCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTCGGTGTGCAC 309

QY 61 CTC 63

Db 310 CTC 312

RESULT 10

AAQ06311

ID AAQ06311 standard; DNA; 3276 BP.

XX AC AAQ06311;

XX DT 25-MAR-2003 (revised)

XX DT 29-JAN-1991 (first entry)

XX DE Sequence of plasmid p238BGL.

XX XW IFN-gamma receptor; autoimmune disease; multiple sclerosis;

XX XX hypersensitivity; ds.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX CDS 243..426

XX /*tag= b

XX /*tag= c

XX /*tag= S.P.1

XX Sig-peptide

XX PI

FT LTR

FT 279..242

FT /*tag= a

FT polyA_signal

FT 585..590

FT /*tag= d

XX PN EP393502-A.

XX PD 24-OCT-1990.

XX PF 11-APR-1990; 90EP-00106992.

XX PR 19-APR-1989; 89EP-00810295.

XX PA (HOFF) HOFFMANN-LA ROCHE AG.

XX PI Fountoulak M, Garotta G, Stuber D;

XX WPI; 1990-322042/43.

XX DR P-PSDB; AAR07066.

XX PT Soluble interferon-gamma receptors - for treating auto-immune diseases,
XX chronic inflammations, etc.

XX PS Disclosure; Fig 51; 174pp; English.

XX CC IFN-gamma is a therapeutically active agent in the treatment of
XX auto-immune disease, allograft transplant rejections, multiple sclerosis,
XX chronic inflammations and delayed hypersensitivity. It is also useful in
XX identifying IFN-gamma agonists and antagonists. See also AAQ06301.
XX (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 3276 BP; 814 A; 794 C; 914 G; 754 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 63; DB 2; Length 3276;

XX Best Local Similarity 100.0%; Pred. No. 3.1e-14;

XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTCGGTGTGCAC 60

Db 250 TTTAAGTCCCTAGCTGATACATAAAGCGCATTTGACCATTCACCATTCGGTGTGCAC 309

QY 61 CTC 63

Db 310 CTC 312

RESULT 11

AAZ93331

ID AAZ93331 standard; DNA; 3310 BP.

XX AC AAZ93331;

XX DT 04-JUL-2000 (first entry)

XX DE Partial sequence of replication deficient adenoviral vector Ad5RSVRed.

XX XW Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;

XX XW Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;

XX XW produg; nicotinamide adenine dinucleotide phosphatase; ss.

XX OS Synthetic.

XX XW WO2000014256-A1.

XX PD 16-MAR-2000.

XX PF 03-SEP-1999; 99WO-US018834.

XX PR 04-SEP-1998; 98US-00148275.

XX PA (GENO-) GENOTHERAPEUTICS INC.

XX PI Steiner MS, Lu Y;

XX DR WPI; 2000-257001/22.

XX PT Replication-deficient adenovirus type 5 expression vectors used for gene

PT therapy of cancer, especially prostate cancer, comprising an insertion of

PT nucleic acid encoding cytochrome p450 genes.

XX PS Disclosure; Fig 10; 110pp; English.

XX PS Claim 18; Fig 11C; 110pp; English.

XX CC Replication-deficient adenovirus type 5 expression vectors comprise an

CC adenovirus genome with a deletion in the E1 and E2 region of the genome

CC and an insertion within the region under the control of a Rous Sarcoma

CC virus promoter can be used to induce chemotoxicity in tumour cells. Three

CC such expression vectors are described, the inserted nucleic acids in each

CC being the following: Vector (I) has an insertion of a nucleic acid

CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-

CC 2628). Vector (II) has an insertion of a nucleic acid encoding a

CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector

CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is

CC designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell

CC can be induced by administering (I) and (III) or (II) and (III) into the

CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell

CC to a prodrug and then administering the prodrug which kills the cell,

CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug

CC therapy to transfer a drug susceptibility gene to the tumor which

CC activates a nontoxic prodrug intratumorally so the released drug can kill

CC the tumor cells containing the drug susceptibility gene. This sequence is

CC designated region A of the vector Ad5RSVRED

XX CC

SQ Sequence 3310 BP; 755 A; 881 C; 980 G; 694 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 3310;

Best Local Similarity 100.0%; Pred. No. 3.1e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60

Db 742 TTTAAGTCCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 801

QY 61 CTC 63

Db 802 CTC 804

RESULT 12

AAZ93079

ID AAZ93079 standard; DNA; 3311 BP.

AC AAZ93079;

DT 04-JUL-2000 (first entry)

DE Partial sequence of replication deficient adenoviral vector Ad5RSVRED.

XX Adenovirus; vector; E1; E3; cytochrome; NADPH cytochrome reductase;

XX Rous Sarcoma virus; RSV; chemotoxicity; transfection; sensitisation;

XX prodrug; nicotinamide adenine dinucleotide phosphatase; ss.

OS Synthetic.

XX W0200014256-A1.

XX PD 16-MAR-2000.

XX PF 03-SEP-1999; 99WO-US018834.

XX PR 04-SEP-1998; 98US-00148275.

XX PA (GENO-) GENOTHERAPEUTICS INC.

XX PI Steiner MS, Lu Y;

XX

DR WPI; 2000-257001/22.

XX PT Replication-deficient adenovirus type 5 expression vectors used for gene

PT therapy of cancer, especially prostate cancer, comprising an insertion of

PT nucleic acid encoding cytochrome p450 genes.

XX PS Claim 18; Fig 11C; 110pp; English.

XX CC Replication-deficient adenovirus type 5 expression vectors comprise an

CC adenovirus genome with a deletion in the E1 and E2 region of the genome

CC and an insertion within the region under the control of a Rous Sarcoma

CC virus promoter can be used to induce chemotoxicity in tumour cells. Three

CC such expression vectors are described, the inserted nucleic acids in each

CC being the following: Vector (I) has an insertion of a nucleic acid

CC encoding a cytochrome 2C9 p450 and is designated Ad5RSV2C9 (ATCC VR-

CC 2628). Vector (II) has an insertion of a nucleic acid encoding a

CC cytochrome 3A4 p450 and is designated Ad5RSV3A4 (ATCC VR-2629). Vector

CC dinucleotide phosphatase (NADPH) cytochrome p450 reductase and is

CC designated Ad5RSVRED (ATCC VR-2630). The chemotoxicity of a tumor cell

CC can be induced by administering (I) and (III) or (II) and (III) into the

CC tumor cell (e.g. a prostate tumor cell) to selectively sensitize the cell

CC to a prodrug and then administering the prodrug which kills the cell,

CC inducing its chemotoxicity. The method uses gene-directed enzyme prodrug

CC therapy to transfer a drug susceptibility gene to the tumor which

CC activates a nontoxic prodrug intratumorally so the released drug can kill

CC the tumor cells containing the drug susceptibility gene. This sequence is

CC designated region A of the vector Ad5RSVRED and is the sequence of the

CC cytochrome NADPH p450 reductase

XX CC

SQ Sequence 3311 BP; 755 A; 881 C; 981 G; 694 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 3311;

Best Local Similarity 100.0%; Pred. No. 3.1e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60

Db 742 TTTAAGTCCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 801

QY 61 CTC 63

Db 802 CTC 804

RESULT 13

AAQ06309

ID AAQ06309 standard; DNA; 3383 BP.

AC AAQ06309;

XX 25-MAR-2003 (revised)

DT 29-JAN-1991 (first entry)

XX Sequence of plasmid p76BGL.

XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;

XX hypersensitivity; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

XX LTR 279..504

XX /*tag= a

XX CDS 505..540

XX /*tag= b

XX polyA_signal 692..697

XX /*tag= c

XX EP393502-A.

XX 24-OCT-1990.

XX

```

PF 11-APR-1990; 90EP-00106992.
XX
XX
PR 19-APR-1989; 89EP-00810295.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Fountoulak M, Garotta G, Stuber D;
XX WPI; 1990-322042/43.
XX P-PSDB; AAR07065.
XX
XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
XX chronic inflammations, etc.
XX Disclosure; Fig 47; 174pp; English.
XX
XX IFN-gamma is a therapeutically active agent in the treatment of
XX autoimmune disease, allograft transplant rejections, multiple sclerosis,
XX chronic inflammations and delayed hypersensitivity. It is also useful in
XX identifying IFN-gamma agonists and antagonists. See also AAQ06301.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 3383 BP; 838 A; 828 C; 929 G; 788 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 63; DB 2; Length 3383;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-14;
XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACACATTGCTGTGCAC 60
DB 250 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACACATTGCTGTGCAC 309
XX
XX 61 CTC 63
XX 310 CTC 312
XX
XX
RESULT 14
AAQ06313
ID AAQ06313 standard; DNA; 3427 BP.
XX
XX AAQ06313;
XX
XX 25-MAR-2003 (revised)
XX 29-JAN-1991 (first entry)
XX
XX Sequence of plasmid p267BGL.
XX
XX IFN-gamma receptor; autoimmune disease; multiple sclerosis;
XX hypersensitivity; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX LTR 279..492
XX /*tag= a
XX CDS 493..585
XX /*tag= b
XX Sig-peptide 493..564
XX /*tag= c
XX polyA_signal /label= S.P.2
XX 736..741
XX /*tag= d
XX
XX EP393502-A.
XX
XX 24-OCT-1990.
XX
XX 11-APR-1990; 90EP-00106992.
XX
XX 19-APR-1989; 89EP-00810295.
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX

```

```

XX Fountoulak M, Garotta G, Stuber D;
XX WPI; 1990-322042/43.
XX P-PSDB; AAR07067.
XX
XX Soluble interferon-gamma receptors - for treating auto-immune diseases,
XX chronic inflammations, etc.
XX Disclosure; Fig 59; 174pp; English.
XX
XX IFN-gamma is a therapeutically active agent in the treatment of
XX autoimmune disease, allograft transplant rejections, multiple sclerosis,
XX chronic inflammations and delayed hypersensitivity. It is also useful in
XX identifying IFN-gamma agonists and antagonists. See also AAQ06301.
XX (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 3427 BP; 846 A; 840 C; 942 G; 799 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 63; DB 2; Length 3427;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-14;
XX Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACACATTGCTGTGCAC 60
DB 250 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCATTCACACATTGCTGTGCAC 309
XX
XX 61 CTC 63
XX 310 CTC 312
XX
XX
RESULT 15
AAC89169
ID AAC89169 standard; DNA; 3885 BP.
XX
XX AAC89169;
XX
XX 08-MAR-2001 (first entry)
XX
XX ADRSVpHYDE region A coding sequence.
XX
XX p-HYDE, cytostatic; gene therapy; apoptosis; leukaemia; prostate;
XX tumour suppressor gene; DNA repair; cancer; melanoma; lymphoma;
XX colorectal; pancreatic; breast; brain; gastric carcinoma; ds.
XX
XX Unidentified.
XX
XX WO2000071564-A2.
XX
XX 30-NOV-2000.
XX
XX 01-MAY-2000; 2000WO-US011456.
XX
XX 29-APR-1999; 99US-00302457.
XX 29-APR-1999; 99US-0131607P.
XX 08-FEB-2000; 2000US-C0499817.
XX
XX (UITE-) UNIV TENNESSEE RES CORP.
XX
XX Steiner MS, Wang C, Rinaldy A, Menon R;
XX WPI; 2001-032016/04.
XX
XX New isolated nucleic acid encoding a mammalian p-Hyde protein of the p-
XX Hyde family is useful for treating cancer, e.g. prostate cancer.
XX
XX Disclosure; Fig 10; 171pp; English.
XX
XX The present sequence is region A of ADRSVpHYDE. ADRSVpHYDE is an
XX adenovirus vector expressing p-HYDE. p-HYDE induces susceptibility of a
XX cancer cell to cell death. The p-HYDE gene is associated with the
XX regression of tumour growth in vivo, the induction to susceptibility to

```


CC apoptosis caused by UV or chemotherapy induced DNA damage and prevention
 CC of DNA repair with the upregulation of apoptosis as the result of UV
 CC damage and the failure to repair DNA. The present sequence may be used to
 CC treat cancer, preferably melanoma, lymphoma, leukaemia, prostate,
 CC colorectal, pancreatic, breast, brain or gastric carcinoma
 XX
 SQ Sequence 3885 BP; 847 A; 1039 C; 1063 G; 936 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 4; Length 3885;
 Best Local Similarity 100.0%; Pred. No. 3.2e-14; Mismatches 0; Indels 0; Gaps 0;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCCTAGCTCGATACATTAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 60
 DB 742 TTTAAGTCCCTAGCTCGATACATTAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 801
 QY 61 CTC 63
 DB 802 CTC 804
 RESULT 16
 AAQ06312
 ID AAQ06312 standard; DNA; 3979 BP.
 XX
 AC AAQ06312;
 XX
 DT 25-MAR-2003 (revised)
 DT 29-JAN-1991 (first entry)
 XX
 DE Sequence of plasmid p264BGL.
 XX
 KW IFN-gamma receptor; autoimmune disease; multiple sclerosis;
 KW hypersensitivity; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 243..426
 FT /*tag= b
 FT Sig-peptide 243..405
 FT /*tag= c
 FT /label= S.P.1
 FT LTR 278..242
 FT /*tag= a
 FT polyA_signal 1288..1292
 FT /*tag= d
 XX
 PN EP393502-A.
 XX
 PD 24-OCT-1990.
 XX
 PF 11-APR-1990; 90EP-00106992.
 XX
 PR 19-APR-1989; 89EP-00810295.
 XX
 EA (HOFF) HOFFMANN-LA ROCHE AG.
 XX
 PI Fountoulak M, Garotta G, Stuber D;
 XX
 DR WPI; 1990-322042/43.
 DR P-PSDB; AAQ07066.
 XX
 FT Soluble interferon-gamma receptors - for treating auto-immune diseases,
 FT chronic inflammations, etc.
 XX
 PS Disclosure; Fig 55; 174pp; English.
 XX
 CC IFN-gamma is a therapeutically active agent in the treatment of
 CC autoimmune disease, allograft transplant rejections, multiple sclerosis,
 CC chronic inflammations and delayed hypersensitivity. It is also useful in
 CC identifying IFN-gamma agonists and antagonists. See also AAQ06301.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC

XX
 SQ Sequence 3979 BP; 947 A; 987 C; 1113 G; 932 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 3979;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14; Mismatches 0; Indels 0; Gaps 0;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCCTAGCTCGATACATTAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 60
 DB 250 TTTAAGTCCCTAGCTCGATACATTAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 309
 QY 61 CTC 63
 DB 310 CTC 312
 RESULT 17
 AAQ75974/c
 ID AAQ75974 standard; cDNA; 4059 BP.
 XX
 AC AAQ75974;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-AUG-1995 (first entry)
 XX
 DE pHLA-B7 expression vector.
 XX
 XX expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
 XX light beta-2 microglobulin; class I major histocompatibility complex;
 XX MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..354
 FT /*tag= a
 FT /note= "pBR322 backbone contg. bacterial origin of
 FT replication"
 FT CDS 355..1170
 FT /*tag= b
 FT /note= "kanamycin resistance gene open reading frame; the
 FT gene is taken from the transposable element Tn903"
 FT polyA_signal complement(1410..1177)
 FT /*tag= c
 FT /note= "SV40 polyA signal sequence"
 FT intron complement(1412..11560)
 FT /*tag= d
 FT /note= "SV40 small t intron"
 FT 3'UTR complement(1561..1794)
 FT /*tag= e
 FT /note= "3' untranslated region of HLA-B7 heavy chain
 FT mRNA"
 FT CDS complement(1795..2880)
 FT /*tag= f
 FT /note= "HLA-B7 open reading frame"
 FT LTR complement(2886..3415)
 FT /*tag= g
 FT /note= "Rous sarcoma virus 3' LTR promoter region"
 FT misc_feature 3416..4059
 FT /*tag= h
 FT /note= "pBR322 backbone"
 XX
 PN M09429469-A2.
 XX
 PD 22-DEC-1994.
 XX
 PF 27-MAY-1994; 94WO-US006069.
 XX
 PR 07-JUN-1993; 93US-00074344.
 XX
 EA (VICA-) VICAL INC.
 PA (UNMI) UNIV MICHIGAN.
 XX

PI Nabel GJ, Nabel EG, Lew D, Marquet M;
 XX DR WPI; 1995-036494/05.
 XX
 PT New vectors for gene therapy, partic for tumours - comprising genetic
 FT material encoding one or more cistron(s) which express immunogenic or
 XX therapeutic peptide(s).
 XX
 PS Claim 9; Page 42-43; 50pp; English.
 XX
 CC This HLA-B7 antigen encoding plasmid was developed to incorporate many
 CC advantageous features, eg. the kanamycin resistance gene. The
 CC eradication of two open reading frames encoding portions of SV40 viral
 CC proteins lowers the risk of tumorigenicity. The vector may also operate
 CC as a cassette into which cistrons may be inserted and removed at will for
 CC the transcription and subsequent translation of peptides of interest. The
 CC vector is used partic. for the treatment of neoplastic disease, eg.
 CC melanoma, and provides enhanced gene delivery and expression in vivo.
 XX (Updated on 25-MAR-2003 to correct PN field.)
 SQ Sequence 4059 BP; 975 A; 1051 C; 1033 G; 1000 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 4059;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACACATTTGGTGTGCAC 60
 Db 2954 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACACATTTGGTGTGCAC 2895
 QY 61 CTC 63
 Db 2894 CTC 2892
 RESULT 18
 AAQ62391
 ID AAQ62391 standard; DNA; 4341 BP.
 XX
 AC AAQ62391;
 XX
 DT 25-MAR-2003 (revised)
 DT 18-NOV-1994 (first entry)
 XX
 DE Vector pVAC1.
 XX
 KW Vector; pVAC1; pRC/RSV; leader sequence; termination signal;
 KW fusion protein; pSfi/NotI/TagI; pElB leader; human; immunoglobulin; VHI;
 KW single chain; Fv; murine antibody; retroviral; envelope; plasmid;
 KW vaccine; ss.
 XX
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT misc_RNA complement(1..775)
 FT /*tag= c
 FT /note= "Claim 9"
 FT misc_RNA 606..780
 FT /*tag= b
 FT /note= "Claim 8"
 FT misc_RNA 606..716
 FT /*tag= a
 FT /note= "Claim 7"
 FT
 XX
 FN WO9408008-A1.
 XX
 PD 14-APR-1994.
 XX
 PF 04-OCT-1993; 93WO-GB002054.
 XX
 PR 02-OCT-1992; 92GB-00020808.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.

XX
 PI Hawkins RE, Russell SJ, Stevenson FK, Winter GP;
 XX DR WPI; 1994-135575/16.
 XX
 PT Modulating immune response to a disease marker - by administering a
 FT vector which expresses the disease marker to interact with the immune
 PT system.
 XX
 PS Claim 10; Fig 7; 77pp; English.
 XX
 CC This sequence represents the vector pVAC1. This vector is based on the
 CC commercially available vector pRC/RSV. Leader sequences and termination
 CC signals were introduced into the vector to allow for production of fusion
 CC proteins. The vector, pSfi/NotI/TagI, was modified to replace the pElB
 CC leader with the human immunoglobulin VHI leader sequence that permits the
 CC encoding of an Sfil cloning site without modification of the amino acid
 CC sequence. This fragment was then cloned as an EcoRI/Blunt-HindIII
 CC fragment into NotI/Blunt- HindIII cut vector pRC/RSV to give pVAC1. The
 CC single chain Fv for an individual patient can be inserted within the VHI
 CC antibody/retroviral envelope fusion protein can be used as a plasmid
 CC vaccine and it induces a strong humoral response to the antibody moiety
 CC in BALB/c mice. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 4341 BP; 1032 A; 1099 C; 1091 G; 1119 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 4341;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACACATTTGGTGTGCAC 60
 Db 542 TTTAAGTGCCTAGCTCGATACATAAAGCGCCATTGACCATTCACACATTTGGTGTGCAC 601
 QY 61 CTC 63
 Db 602 CTC 604
 RESULT 19
 AAS17704
 ID AAS17704 standard; DNA; 4341 BP.
 XX
 AC AAS17704;
 XX
 DT 12-MAR-2002 (first entry)
 DE Vector pVAC1 encoding a DNA vaccine.
 XX
 KW Cytostatic; vaccine; tetanus toxin; FrC; tumour; CTL; PCR primer; pVAC1;
 KW ds.
 XX
 OS Clostridium tetani.
 OS Homo sapiens.
 OS Synthetic.
 OS Cauliflower mosaic virus.
 XX
 FN WO200179510-A1.
 XX
 PD 25-OCT-2001.
 XX
 PF 17-APR-2001; 2001WO-GE001719.
 XX
 PR 17-APR-2000; 2000GB-00009470.
 XX
 PA (CANC-) CANCER RES VENTURES LTD.
 XX
 PI Rice J, Stevenson F;
 XX DR WPI; 2002-066370/09.
 XX
 FT Nucleic acid construct, useful to immunize against various diseases

PT including cancer, expresses the first domain of tetanus toxin Frc fused
 XX to a disease peptide antigen to provide a vaccine.
 PS Disclosure; Fig 4; 71pp; English.
 XX
 CC The invention relates to a nucleic acid construct for delivery into
 CC living cells in vivo, to induce an immune response to a disease peptide
 CC antigen, where the construct directs expression of a fusion protein
 CC comprising the peptide antigen and the first domain of Frc. Also included
 CC are a nucleic acid vector comprising the above construct, a host cell
 CC comprising the above construct or vector and a method of producing a
 CC nucleic acid construct for inducing an immune response. The method
 CC comprises identifying a nucleic acid sequence encoding a disease peptide
 CC antigen comprising epitopes characteristic of the disease, cloning the
 CC nucleic acid sequence, introducing the cloned nucleic acid into a vector
 CC which allows the antigen to be expressed as a fusion with a first domain
 CC Frc from tetanus toxin, and optionally isolating the construct from the
 CC vector. The construct or vector is used as a vaccine to induce an immune
 CC response, particularly to tumour antigens. The present sequence is vector
 CC pVAC1 which encodes a vaccine of the invention
 XX
 SQ Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 6; Length 4341;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTTCACCATTCACCATTCGTTGGTGCAC 60
 Db |||||
 542 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTTCACCATTCACCATTCGTTGGTGCAC 601
 QY 61 CTC 63
 Db |||
 602 CTC 604
 RESULT 20
 ABN83143
 ID ABN83143 standard; DNA; 4341 BP.
 XX
 AC ABN83143;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Plasmid pVAC1 complete sequence.
 XX
 KW Immune response; plant viral coat protein; pVAC1; cytostatic; virucide;
 KW cancer; B cell malignancy; ds.
 XX
 OS Synthetic.
 XX
 XX WO200240513-A2.
 XX
 XX 23-MAY-2002.
 XX
 XX 20-NOV-2001; 2001WO-GB005142.
 XX
 XX 20-NOV-2000; 2000GB-00028319.
 XX
 XX (CANC-) CANCER RES VENTURES LTD.
 XX
 XX Savelyeva N, Stevenson F;
 XX
 XX WPI; 2002-500202/53.
 XX
 XX Nucleic acid construct for delivery into living cells as a vaccine,
 PT useful for treating e.g. cancer, directs the expression of a fusion
 PT protein comprising an antigen and an adjuvant sequence derived from a
 PT plant viral coat protein.
 XX
 XX Example 3; Fig 7; 84pp; English.
 XX
 CC The invention relates to a novel nucleic acid construct for inducing an

CC immune response in vivo to an antigen, capable of directing the
 CC expression of a fusion protein that comprises an antigen and an adjuvant
 CC sequence derived from a plant viral coat protein. The construct of the
 CC invention has cytostatic and virucide activity. The nucleic acid
 CC construct is useful for inducing an immune response in a patient, for
 CC vaccinating a patient against an infectious disease caused by an antigen
 CC derived from a pathogen e.g. a virus, for treating a cancer patient or a
 CC patient with a predisposition to cancer and for treating a patient having
 CC a B cell malignancy, where the construct is encapsidated, and optionally,
 CC a second nucleic acid sequence encoding a further immunomodulatory
 CC polypeptide is administered to the patient. The construct is also useful
 CC in medical treatment, and in the preparation of a vaccine for treating or
 CC preventing a disease state associated with the antigen. The sequence
 CC shows the complete sequence of vector pVAC1
 XX
 SQ Sequence 4341 BP; 1033 A; 1099 C; 1090 G; 1119 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 6; Length 4341;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTTCACCATTCACCATTCGTTGGTGCAC 60
 Db |||||
 542 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTTCACCATTCACCATTCGTTGGTGCAC 601
 QY 61 CTC 63
 Db |||
 602 CTC 604
 RESULT 21
 ADD35599
 ID ADD35599 standard; DNA; 4457 BP.
 XX
 XX AC ADD35599;
 XX
 XX 15-JAN-2004 (first entry)
 XX
 XX Bicistronic eukaryotic expression vector Pl178.
 XX
 KW Multicistronic eukaryotic expression vector; multiple protein expression;
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
 KW chain terminator; transcription pause site; gene transfer;
 KW DNA immunisation; gene therapy; Pl178; kanamycin resistance gene;
 KW Rous sarcoma virus; RSV promoter; Pl178; rabbit beta-globin intron;
 KW hepatitis C virus; HCV IRES; mRSG terminator; cyclic; circular; ds.
 XX
 OS Chimeric.
 OS Synthetic.
 OS Rous sarcoma virus.
 OS Oryctolagus cuniculus.
 OS Hepatitis C virus.
 OS Escherichia coli.
 XX
 XX WO2003031630-A1.
 XX
 XX 17-APR-2003.
 XX
 XX 10-OCT-2002; 2002WO-IT000646.
 XX
 XX 12-OCT-2001; 2001IT-MI002110.
 XX
 XX (KERY-) KERYOS SPA.
 XX
 XX Pazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
 XX
 XX WPI; 2003-393446/37.
 XX
 XX New multicistronic recombinant plasmid vectors expressing two to our
 PT genes simultaneously, useful in various biotechnological applications,
 PT such as gene transfer, gene therapy and in DNA immunization.
 XX
 XX Claim 18; SEQ ID NO 2; 52pp; English.
 PS

XX The invention relates to multicistronic eukaryotic expression vectors for
 CC the expression of at least two proteins of interest which may be
 CC identical or different. The vectors comprise at least one eukaryotic
 CC expression cassette having a promoter/enhancer sequence, an intron
 CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
 CC and a chain terminator. The vectors may additionally contain a
 CC transcription pause site downstream of the chain terminator. The
 CC invention also encompasses eukaryotic host cells comprising a vector of
 CC the invention, and the recombinant expression of two or more eukaryotic
 CC proteins using host cells transformed with a vector of the invention.
 CC The vectors are useful in various biotechnological applications in which
 CC the simultaneous expression of two or more genes is necessary, such as
 CC gene transfer protocols, DNA immunisation, or for the expression of
 CC different molecules in the same cell. They may also be used in gene
 CC therapy. The present sequence represents a specifically claimed vector
 CC designated PL178, which comprises a Rous sarcoma virus (RSV) promoter,
 CC rabbit beta-globin intron, the hepatitis C virus (HCV) IRES, and a rabbit
 CC beta-globin gene mRGS terminator as well as a kanamycin resistance gene.
 XX
 SQ Sequence 4457 BP; 1095 A; 1027 C; 1123 G; 1212 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 9; Length 4457;
 Best Local Similarity 100.0%; Pred. No. 3.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
 DB 918 TTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 977
 QY 61 CTC 63
 DB 978 CTC 980

RESULT 22
 AAA09085
 ID AAA09085 standard; DNA; 4487 BP.
 XX
 AC AAA09085;
 DT 15-SEP-2003 (revised)
 DT 06-AUG-2003 (revised)
 DT 10-AUG-2000 (first entry)
 XX
 DE ADRSV-beta-galactosidase vector region A.
 XX
 KW Region A; replication-deficient; vector; lacZ; beta-galactosidase;
 KW Rous Sarcoma Virus; RSV; promoter; cytotoxicity; cytostatic; pro-drug;
 KW prostate cancer; gene therapy; ss.
 XX
 OS Human adenovirus type 5.
 OS Rous sarcoma virus.
 OS Escherichia coli.
 OS Chimeric.
 XX
 FN WO2000020038-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 01-OCT-1999; 99WO-US020907.
 XX
 PR 02-OCT-1998; 98US-00165730.
 XX
 PA (GENO-) GENOTHERAPEUTICS INC.
 XX
 PI Steiner MS;
 XX
 DR WPI; 2000-303646/26.
 XX
 PT Inducing cellular cytotoxicity of tumor cell comprises introducing
 PT replication-deficient adenovirus type 5 expression vector containing gene
 PT encoding for enzyme having ability to convert nontoxic prodrug into

PT cancer killing drug.
 XX
 PS Claim 4; Fig 18B; 178pp; English.
 XX
 CC This sequence comprises Region A of a replication-deficient adenovirus
 CC type 5 vector containing a lacZ gene (encoding beta-galactosidase (beta-
 CC gal)) under the control of the Rous Sarcoma Virus (RSV) promoter.
 CC Inducing cellular cytotoxicity of a tumor cell comprises introducing a
 CC replication-deficient adenovirus type 5 expression vector comprising a
 CC gene that encodes for an enzyme that has the ability to convert a non-
 CC toxic pro-drug into a cancer killing drug which then destroys cancer
 CC cells. The adenovirus genome preferably has a deletion in an E1 and E3
 CC region and an insertion within the region of a nucleic acid encoding
 CC Escherichia coli beta-gal under the control of a promoter. The pro-drug
 CC active site is masked by beta-gal. Functional beta-gal is expressed from
 CC the vector so as to activate the pro-drug into an agent toxic to the
 CC cells. Beta-gal can be under the control of an RSV, probasin (PB),
 CC Prostate Specific Antigen (PSA) or Mouse Mammary Tumor Virus (MMTV)
 CC promoter. The vectors provide a novel way to treat prostate cancer by
 CC gene therapy. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
 CC 15-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 4487 BP; 1031 A; 1148 C; 1288 G; 1020 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 4487;
 Best Local Similarity 100.0%; Pred. No. 3.4e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 60
 DB 742 TTTAAGTCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 801
 QY 61 CTC 63
 DB 802 CTC 804

RESULT 23
 AAAT02998
 ID AAAT02998 standard; DNA; 5653 BP.
 XX
 AC AAAT02998;
 XX
 DT 24-MAR-1996 (first entry)
 DT
 XX
 DE RSV tar Rev M10 expression plasmid pRSVtarRevM10.
 XX
 KW Plasmid pRSVtarRevM10; particle-mediated gene transfer; cyclic;
 KW particle acceleration; HIV virus infection; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..36
 FT /tag= a
 FT /note= "pBR322 vector sequence"
 FT enhancer 37..610
 FT /tag= b
 FT /note= "RSV enhancer"
 FT promoter 611..699
 FT /tag= c
 FT /label= tar
 FT /note= "HIV promoter tat responsive element"
 FT mat_peptide 700..1129
 FT /tag= d
 FT /note= "Rev M10 open reading frame"
 FT polyA_signal 1243
 FT /tag= e
 FT /note= "cattle somatotropin poly(A) site"
 FT promoter 1993..2300
 FT /tag= f
 FT /note= "pSVneo promoter"
 FT misc_feature 2346

```

FT      /tag= g
FT      /label= kanamycin_resistance_gene
FT      /note= "pSV2 neo selectable marker gene"
FT      3360
FT      polyA_signal
FT      /tag= h
FT      /note= "pSV2 neo"
FT      3459..5653
FT      /tag= i
FT      /note= "plasmid pUC ori/amp sequence"
FT
XX      WO9529703-A1.
XX
XX      09-NOV-1995.
XX
XX      01-MAY-1995; 95WO-US005024.
XX
XX      29-APR-1994; 94US-00235277.
XX
XX      (NABE/) NABEL G J.
XX      (WOFF/) WOFFENDIN C.
XX      (YANG/) YANG N.
XX      (SHEE/) SHEEHY M J.
XX
XX      Nabel GJ, Woffendin C, Yang N, Sheehy MJ;
XX      WPI; 1995-403807/51.
XX
XX      Particle-mediated gene transfer - in T cells, monocytes, macrophage(s),
XX      dendrites or haematopoietic stem cells, partic. for treating HIV
XX      infection.
XX
XX      Disclosure; Fig 11a-11e; 96pp; English.
XX
XX      Expression plasmid pSVtRevM10 contains the Rev M10 HIV protective gene
XX      (a dominant-negative inhibition gene) under the control of the Tat
XX      sequence (HIV promoter -18 to -72), i.e. gene expression is activated by
XX      Tat. The plasmid also contains the kanamycin- resistance selectable
XX      marker gene. The plasmid is used in a particle-mediated gene transfer
XX      process for Rev M10 gene expression in T-cells (preferably), monocytes,
XX      macrophages, haematopoietic stem cells or dendrites. The gold
XX      microparticle acceleration process results in stable incorporation of
XX      foreign genes in the cells. This method is used to treat HIV infection.
XX      Rev M10 transduced cells are resistant to HIV challenge. The method may
XX      be applied to the transfer of other therapeutic genes in a gene therapy
XX      process
XX
XX      Sequence 5653 BP; 1328 A; 1428 C; 1478 G; 1419 T; 0 U; 0 Other;
XX
XX      Query Match 100.0%; Score 63; DB 2; Length 5653;
XX      Best Local Similarity 100.0%; Pred. No. 3.5e-14;
XX      Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 1 TTTAAGTGGCTAGTCGATACATTAAGCCCATTTGACCATTCACCATTTGGTGGCAC 60
XX      |||||
XX      Db 542 TTTAAGTGGCTAGTCGATACATTAAGCCCATTTGACCATTCACCATTTGGTGGCAC 601
XX
XX      QY 61 CTC 63
XX      |||
XX      Db 602 CTC 604

RESULT 24
AAT76802
ID AAT76802 standard; DNA; 5653 BP.
XX
XX      AC AAT76802;
XX
XX      18-NOV-1997 (first entry)
XX
XX      RSV tar Rev m10 retroviral vector DNA sequence.
XX
XX      inhibit; Human Immunodeficiency Virus; HIV; gene expression;
XX      transcription activation region; TAR; negative transdominant mutant;
XX

```

```

KW      Rev M10; mutant; nuclear protein; viral regulatory protein; tat;
KW      RSV tar Rev M10 plasmid; Rous sarcoma virus; RSV; ds.
XX
XX      Synthetic.
XX
XX      Key Location/Qualifiers
XX      enhancer 37..1129
XX      /tag= b
XX      /note= "expression control sequence, contains Rous
XX      Sarcoma Virus enhancer and Rev M10 gene"
XX      700..1129
XX      /tag= a
XX      /note= "Rev M10 gene"
XX
XX      US5650306-A.
XX
XX      22-JUL-1997.
XX
XX      07-JUN-1993; 93US-00073836.
XX
XX      07-JUN-1993; 93US-00073836.
XX
XX      (UNMI ) UNIV MICHIGAN.
XX
XX      Woffendin C, Liu J, Nabel GJ, Yang Z;
XX      WPI; 1997-384672/35.
XX
XX      Recombinant nucleic acid for inhibiting HIV gene expression - comprises
XX      expression control sequence and transcription activation region linked to
XX      rev negative trans:dominant mutant gene.
XX
XX      Claim 7; Fig 7; 35pp; English.
XX
XX      Recombinant nucleic acid molecules for the improved expression of genes
XX      which inhibit Human Immunodeficiency Virus (HIV) gene expression are
XX      claimed, which comprise an expression control sequence and a
XX      transcription activation region (TAR) sequence, operatively linked to a
XX      negative transdominant mutant gene (a protective gene), where the
XX      negative transdominant mutant gene is a mutant of rev. Rev is an 18 kDa
XX      nuclear viral regulatory protein in HIV gene expression which controls
XX      export of viral RNA from the nucleus to the cytoplasm of infected cells.
XX      The TAR sequence which is found in the HIV genome controls the regulatory
XX      activity of the tat protein. The TAR sequence is linked to the protective
XX      gene, and therefore controls its expression. This sequence is a preferred
XX      recombinant nucleic acid vector, designated RSV tar Rev M10 plasmid
XX
XX      Sequence 5653 BP; 1326 A; 1429 C; 1478 G; 1420 T; 0 U; 0 Other;
XX
XX      Query Match 100.0%; Score 63; DB 2; Length 5653;
XX      Best Local Similarity 100.0%; Pred. No. 3.5e-14;
XX      Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 1 TTTAAGTGGCTAGTCGATACATTAAGCCCATTTGACCATTCACCATTTGGTGGCAC 60
XX      |||||
XX      Db 542 TTTAAGTGGCTAGTCGATACATTAAGCCCATTTGACCATTCACCATTTGGTGGCAC 601
XX
XX      QY 61 CTC 63
XX      |||
XX      Db 602 CTC 604

RESULT 25
AAQ43814
ID AAQ43814 standard; DNA; 5750 BP.
XX
XX      AC AAQ43814;
XX
XX      25-MAR-2003 (revised)
XX      20-OCT-1993 (first entry)
XX
XX      pRLD3D4 construct.
XX

```

KW Epidermal growth factor receptor truncate protein; EGF; binding sites;
 KW adsorptive agents; mammalian cell growth abnormality; detection; growth;
 KW reproduction; signal transmission; ds.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT misc_feature 1077..1079
 FT /*tag= a
 FT /note= "codon ARA encodes Ile"
 XX
 XX US5218090-A.
 XX
 XX 08-JUN-1993.
 XX
 XX 26-OCT-1990; 90US-00604728.
 XX
 XX 12-JUN-1990; 90US-00536896.
 XX
 XX (WARN) WARNER LAMBERT CO.
 XX
 XX Connors RW;
 XX
 XX WPI; 1993-196297/24.
 XX P-PSDB; AAR38211.
 XX
 XX New epidermal growth factor receptor truncate proteins - which bind
 XX ligands of EGF receptor without transmitting signal for growth or
 XX reproduction.
 XX
 XX Disclosure; Fig 9; 42pp; English.
 XX
 XX The sequence is that of the PRLD3D4 construct which encodes the epidermal
 XX growth factor (EGF) receptor truncate protein LN3D4 having EGF binding
 XX sites. The protein binds ligands of the EGF receptor without transmitting
 XX a signal for the growth and reproduction of a cell. It can be used as an
 XX adsorptive agent for any moieties that bind the EGF receptor as the
 XX portal of entry to a cell. It competes with the EGF receptor present on
 XX the cell surface for the binding of ligands and thereby inhibits the
 XX action of the ligands or prevents the entry of viruses into cells. It can
 XX also be used as for the EGF receptor itself, such as in the detection of
 XX abnormalities in mammalian cell growth. It is also useful for prepreg.
 XX agonists or agonists. The features table indicate a discrepancy between
 XX the LN3D4 protein sequence given in the specification and that which the
 XX PRLD3D4 DNA sequence given in the specification would encode. (Updated on
 XX 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 5750 BP; 1367 A; 1479 C; 1536 G; 1367 T; 0 U; 1 Other;
 SQ
 Query Match 100.0%; Score 63; DB 2; Length 5750;
 Best Local Similarity 100.0%; Pred. No. 3.5e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 Db 542 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 601
 QY 61 CTC 63
 Db 602 CTC 604
 RESULT 26
 ID AAQ43813
 XX AAQ43813;
 XX
 XX 25-MAR-2003 (revised)
 DT 20-OCT-1993 (first entry)
 XX
 XX PRLD2D3D4 construct.
 DE

XX
 KW Epidermal growth factor receptor truncate protein; EGF; binding sites;
 KW adsorptive agents; mammalian cell growth abnormality; detection; growth;
 KW reproduction; signal transmission; ds.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT misc_feature 665..2193
 FT /*tag= a
 FT /codon= 707-708 CG encodes Ile
 FT /note= "encodes LD2D3D4"
 FT 1519..1521
 FT /*tag= b
 FT /note= "codon ARA encodes Ile"
 XX
 XX US5218090-A.
 XX
 XX 08-JUN-1993.
 XX
 XX 26-OCT-1990; 90US-00604728.
 XX
 XX 12-JUN-1990; 90US-00536896.
 XX
 XX (WARN) WARNER LAMBERT CO.
 XX
 XX Connors RW;
 XX
 XX WPI; 1993-196297/24.
 XX P-PSDB; AAR38210.
 XX
 XX New epidermal growth factor receptor truncate proteins - which bind
 XX ligands of EGF receptor without transmitting signal for growth or
 XX reproduction.
 XX
 XX Disclosure; Fig 6; 42pp; English.
 XX
 XX The sequence is that of the PRLD2D3D4 construct which encodes the
 XX epidermal growth factor (EGF) receptor truncate protein LD2D3D4 having
 XX EGF binding sites. The protein binds ligands of the EGF receptor without
 XX transmitting a signal for the growth and reproduction of a cell. It can
 XX be used as an adsorptive agent for any moieties that bind the EGF
 XX receptor as the portal of entry to a cell. It competes with the EGF
 XX receptor present on the cell surface for the binding of ligands and
 XX thereby inhibits the action of the ligands or prevents the entry of
 XX viruses into cells. It can also be used as for the EGF receptor itself,
 XX such as in the detection of abnormalities in mammalian cell growth. It is
 XX also useful for prepreg. novel receptors for efficient detection of ligands
 XX and their anti-agonists or agonists. The features table indicates the
 XX discrepancies between the LD2D3D4 protein sequence given in the
 XX specification and that which the PRLD2D3D4 DNA sequence given in the
 XX specification would encode. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 6207 BP; 1474 A; 1620 C; 1670 G; 1442 T; 0 U; 1 Other;
 SQ
 Query Match 100.0%; Score 63; DB 2; Length 6207;
 Best Local Similarity 100.0%; Pred. No. 3.6e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 Db 542 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 601
 QY 61 CTC 63
 Db 602 CTC 604
 RESULT 27
 ID AAQ43812
 XX AAQ43812 standard; DNA; 6274 BP.
 XX
 XX AAQ43812;
 AC

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XX 25-MAR-2003 (revised)
DT 20-OCT-1993 (first entry)
XX
XX pRLD1D2D3_ApaI construct.
XX
XX Epidermal growth factor receptor truncate protein; EGF; growth;
KW binding sites; adsorptive agents; mammalian cell growth abnormality;
KW detection; reproduction; signal transmission; pRLD1D2D3_ApaI; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 665..2253
XX /*tag= a
XX /codon= 707-708 CG encodes Ile
XX /*note= "encodes LD1D2D3_ApaI"
XX misc_feature 1939..1941
XX /*tag= b
XX /*note= "codon AEA encodes Ile"
XX
XX US5218090-A.
XX
XX 08-JUN-1993.
XX
XX 26-OCT-1990; 90US-00604728.
XX
XX 12-JUN-1990; 90US-00536896.
XX
XX (WARN ) WARNER LAMBERT CO.
XX
XX Connors RW;
XX
XX WPI; 1993-196297/24.
DR P-PSDB; AAR38209.
XX
XX New epidermal growth factor receptor truncate proteins - which bind
XX ligands of EGF receptor without transmitting signal for growth or
XX reproduction.
XX
XX Disclosure; Fig 3; 42pp; English.
XX
XX The sequence is that of the pRLD1D2D3 construct which encodes the
XX epidermal growth factor (EGF) receptor truncate protein LD1D2D3_ApaI
XX having EGF binding sites. The protein binds ligands of the EGF receptor
XX without transmitting a signal for the growth and reproduction of a cell.
XX It can be used as an adsorptive agent for any moieties that bind the EGF
XX receptor as the portal of entry to a cell. It competes with the EGF
XX receptor present on the cell surface for the binding of ligands and
XX thereby inhibits the action of the ligands or prevents the entry of
XX viruses into cells. It can also be used as for the EGF receptor itself,
XX such as in the detection of abnormalities in mammalian cell growth. It is
XX also useful for prep. novel receptors for efficient detection of ligands
XX and their anti-agonists or agonists. The features table indicates the
XX discrepancies between the LD1D2D3 protein sequence given in the
XX specification and that which the pRLD1D2D3 DNA sequence given in the
XX specification would encode. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 6274 BP; 1506 A; 1610 C; 1664 G; 1493 T; 0 U; 1 Other;
SQ
Query Match 100.0%; Score 63; DB 2; Length 6274;
Best Local Similarity 100.0%; Pred. No. 3.6e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTAAGTCCTAGCTCGATACATTAACCGCATTTGACCATTCACACATTGGTGTGCAC 60
Db 542 TTTAAGTCCTAGCTCGATACATTAACCGCATTTGACCATTCACACATTGGTGTGCAC 601
Qy 61 CTC 63
Db 602 CTC 604

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RESULT 28
AAAS3869
ID AAAS3869 standard; DNA; 6838 BP.
XX
XX AAAS3869;
XX
XX 03-JAN-2001 (first entry)
XX
XX Expression vector pRIG-1.
XX
XX Vector; endogenous gene; activation; over-expression; erythropoietin;
KW growth hormone; drug discovery; granulocyte colony stimulating factor;
XX ds.
XX
XX Synthetic.
XX
XX W0200049162-A2.
XX
XX 24-AUG-2000.
XX
XX 22-FEB-2000; 2000WO-US0004429.
XX
XX 19-FEB-1999; 99US-00253022.
XX
XX 08-MAR-1999; 99US-00263814.
XX
XX 26-MAR-1999; 99US-00276820.
XX
XX (ATHE-) ATHERSYS INC.
XX
XX Harrington JJ, Sherf B, Rundlett S;
XX
XX WPI; 2000-549276/50.
XX
XX Non-targeted activation of endogenous genes, e.g. for the production of
XX erythropoietin, growth hormone or granulocyte-colony stimulating factor
XX proteins and for drug discovery.
XX
XX Example 1; Fig 14; 240pp; English.
XX
XX New methods, vectors and cells are described for non-targeted activation
XX and over-expression of endogenous genes. The vector constructs comprise
XX transcriptional regulatory sequences (TRS) and unpaired splice donor
XX sequences (USDS), preferably the vectors comprise (in sequential order) a
XX TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
XX site (LS) with a second TRS linked to a selectable marker (SM) lacking a
XX polyadenylation signal. The methods, vectors and cells comprising the
XX vectors may be used for the non-targeted activation and over-expression
XX of endogenous genes, e.g. for the production of proteins (including
XX erythropoietin, growth hormone or granulocyte-colony stimulating factor)
XX and drug discovery. The advantage of these methods are that endogenous
XX genes including those associated with human disease and development, may
XX be activated and isolated without prior knowledge of the sequence
XX structure, function or expression profile of the genes being known
XX
XX Sequence 6838 BP; 1679 A; 1669 C; 1709 G; 1781 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 63; DB 3; Length 6838;
Best Local Similarity 100.0%; Pred. No. 3.7e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTAAGTCCTAGCTCGATACATTAACCGCATTTGACCATTCACACATTGGTGTGCAC 60
Db 1761 TTTAAGTCCTAGCTCGATACATTAACCGCATTTGACCATTCACACATTGGTGTGCAC 1820
Qy 61 CTC 63
Db 1821 CTC 1823

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RESULT 29
AAT12662
ID AAT12662 standard; cDNA; 6926 BP.
XX
XX AAT12662;
AC

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XX 09-MAY-1996 (first entry)
 XX IL-4.Y124D/IgG1 fusion DNA in vector pDB951.
 DE Interleukin-4; interleukin-13; antagonist; IL-4; IL-13; immunoglobulin;
 XX IgG; constant domain; allergy; autoimmune disease; chronic infection;
 KW IL4.Y124D/IgG1; fusion protein; therapy; vector; COSFclink; pDB951; ss.
 XX Synthetic.
 OS WO9604388-A1.
 XX 15-FEB-1996.
 XX 28-JUL-1995; 95WO-EP003036.
 XX 29-JUL-1994; 94GB-00015379.
 PR 06-JUN-1995; 95US-00468297.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX Browne MJ, Murphy KB, Chapman CG, Clinkenbeard HE, Young PR;
 PI Shatzman AB;
 XX WPI; 1996-129404/13.
 XX New soluble protein antagonists of interleukin-4 and interleukin-13 -
 PT comprise IL-4 mutant fused to Ig constant domain, useful in treating e.g.
 PT allergy, autoimmune disease or chronic infection.
 XX Example 1; Page 23-25; 35pp; English.
 XX Vector plasmid pDB951 (AA112662) is derived from the COSFclink vector
 CC (AA112661) and contains a fusion gene (AA112658) coding for a human
 CC interleukin-4(Y124D) mutant-human IgG4 constant region fusion protein
 CC (AA190920). HeLa cells transfected by the vector produce soluble fusion
 CC protein showing IL-4 antagonist activity
 XX Sequence 6926 BP; 1890 A; 1698 C; 1679 G; 1659 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 63; DB 2; Length 6926;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTGCAC 60
 Db 709 TTTAAGTCCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTGCAC 768
 QY 61 CTC 63
 Db 769 CTC 771
 RESULT 30
 ADD35600/c
 ID ADD35600 standard; DNA; 7086 BP.
 XX ADD35600;
 XX 15-JAN-2004 (first entry)
 XX Tricistronic eukaryotic expression vector PL249.
 DE Multicistronic eukaryotic expression vector; multiple protein expression;
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
 KW chain terminator; transcription pause site; gene transfer;
 KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;
 KW cytomagalovirus; CMV promoter/enhancer; CMV intron A;
 KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
 KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
 KW mRGS terminator; cyclic; circular; ds.

XX Chimeric.
 OS Synthetic.
 OS Human herpesvirus 5.
 OS Encephalomyocarditis virus.
 OS Simian virus 40.
 OS Rous sarcoma virus.
 OS Oryctolagus cuniculus.
 OS Escherichia coli.
 XX WO2003031630-A1.
 XX 17-APR-2003.
 XX 10-OCT-2002; 2002WO-ITU00646.
 XX 12-OCT-2001; 2001IT-MI002110.
 XX (KERY-) KERYOS SPA.
 XX Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
 XX WPI; 2003-393446/37.
 XX New multicistronic recombinant plasmid vectors expressing two to our
 PT genes simultaneously, useful in various biotechnological applications,
 PT such as gene transfer, gene therapy and in DNA immunization.
 XX Claim 18; SEQ ID NO 3; 52pp; English.
 XX The invention relates to multicistronic eukaryotic expression vectors for
 CC the expression of at least two proteins of interest which may be
 CC identical or different. The vectors comprise at least one eukaryotic
 CC expression cassette having a promoter/enhancer sequence, an intron
 CC and a cloning site, a viral internal ribosomal entry site (IRES)
 CC and a chain terminator. The vectors may additionally contain a
 CC transcription pause site downstream of the chain terminator. The
 CC invention also encompasses eukaryotic host cells comprising a vector of
 CC the invention, and the recombinant expression of two or more eukaryotic
 CC proteins using host cells transformed with a vector of the invention.
 CC The vectors are useful in various biotechnological applications in which
 CC the simultaneous expression of two or more genes is necessary, such as
 CC gene transfer protocols, DNA immunisation, or for the expression of
 CC different molecules in the same cell. They may also be used in gene
 CC therapy. The present sequence represents a specifically claimed vector
 CC designated PL249, which comprises a cytomagalovirus (CMV)
 CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
 CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous
 CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, and a rabbit
 CC beta-globin gene mRGS terminator as well as a kanamycin resistance gene.
 XX Sequence 7086 BP; 1870 A; 1699 C; 1753 G; 1764 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 63; DB 9; Length 7086;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGTTGTGCAC 60
 Db 1595 TTTAAGTCCTAGCTCGATACATAAAGCCATTTCACCATTCGTTGTGCAC 1536
 QY 61 CTC 63
 Db 1535 CTC 1533
 RESULT 31
 ADD35601/c
 ID ADD35601 standard; DNA; 7334 BP.
 XX ADD35601;
 XX 15-JAN-2004 (first entry)

XX DE Tetracistronic eukaryotic expression vector PL250.

XX KW Multicistronic eukaryotic expression vector; multiple protein expression;
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
 KW chain terminator; transcription pause site; gene transfer;
 KW DNA immunisation; gene therapy; P190; kanamycin resistance gene;
 KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
 KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
 KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
 KW hepatitis C virus; HCV IRES; MRGB terminator; cyclic; circular; ds.
 XX OS Chimeric.
 OS Synthetic.
 OS Human herpesvirus 5.
 OS Encephalomyocarditis virus.
 OS Simian virus 40.
 OS Rous sarcoma virus.
 OS Oryctolagus cuniculus.
 OS Hepatitis C virus.
 OS Escherichia coli.
 XX WO2003031630-A1.
 XX 17-APR-2003.
 XX 10-OCT-2002; 2002WO-IT000646.
 XX 12-OCT-2001; 2001IT-MI002110.
 XX (KERY-) KERYOS SPA.
 XX Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
 XX WPI; 2003-393446/37.
 XX New multicistronic recombinant plasmid vectors expressing two to our
 PT genes simultaneously, useful in various biotechnological applications,
 PT such as gene transfer, gene therapy and in DNA immunization.
 XX Claim 18; SEQ ID NO 4; 52pp; English.

XX The invention relates to multicistronic eukaryotic expression vectors for
 CC the expression of at least two proteins of interest which may be
 CC identical or different. The vectors comprise at least one eukaryotic
 CC expression cassette having a promoter/enhancer sequence, an intron
 CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
 CC and a chain terminator. The vectors may additionally contain a
 CC transcription pause site downstream of the chain terminator. The
 CC invention also encompasses eukaryotic host cells comprising a vector of
 CC the invention, and the recombinant expression of two or more eukaryotic
 CC proteins using host cells transformed with a vector of the invention.
 CC The vectors are useful in various biotechnological applications in which
 CC the simultaneous expression of two or more genes is necessary, such as
 CC gene transfer protocols, DNA immunisation, or for the expression of
 CC different molecules in the same cell. They may also be used in gene
 CC therapy. The present sequence represents a specifically claimed vector
 CC designated PL250, which comprises a cytomegalovirus (CMV)
 CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
 CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous
 CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, the hepatitis C
 CC virus (HCV) IRES, and a rabbit beta-globin gene MRGB terminator as well
 CC as a kanamycin resistance gene.

SQ Sequence 7334 BP; 1922 A; 1775 C; 1825 G; 1812 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 9; Length 7334;
 Best Local Similarity 100.0%; Pred. No. 3.7e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGGAC 60
 DB 1839 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGGAC 1780

QY 61 CTC 63
 DB 1779 CTC 1777

RESULT 32
 AAZ45929
 ID AAZ45929 standard; DNA; 7492 BP.
 XX AC AAZ45929;
 XX 25-APR-2000 (first entry)
 XX Nucleotide sequence of the vector p43C-AT-IN.
 XX Viral vector; p43C-AT-IN; alpha-1-antitrypsin; gene therapy; diabetes;
 KW alpha-1-antitrypsin deficiency; haemophilia; neurological disorder;
 KW adenosine deaminase deficiency; autoimmune disease; interleukin-2;
 KW immunodeficiency disease; infection; cytokine; circular; cancer; ss.
 XX Synthetic.
 OS Adeno-associated virus.
 OS Homo sapiens.
 XX WO9955564-A1.
 XX 04-NOV-1999.
 XX 23-APR-1999; 99WO-US008921.
 XX 24-APR-1998; 98US-0083025P.
 XX (UYFL) UNIV FLORIDA.
 XX Flotte TR, Song S, Byrnes BJ, Morgan M;
 WPI; 2000-147020/13.
 XX Recombinant viral vector useful in the gene therapy of alpha-1-
 PT antitrypsin deficiency and also in hemophilia and diabetes.
 XX Claim 32; Fig 19A-C; 85pp; English.

XX The present sequence represents a recombinant viral vector, designated
 CC p43C-AT-IN, which encodes human alpha-1-antitrypsin protein, and which is
 CC derived from vector p43C-AT by insertion of intron II sequence of the
 CC human alpha-1-antitrypsin gene into the human alpha-1-antitrypsin cDNA.
 CC The vector is exemplary of the vectors of the invention which comprise a
 CC polynucleotide encoding a protein, and are used for gene therapy to
 CC correct genetic disorders related to expression of a protein of interest.
 CC The vectors of the invention are based on Adeno associated virus (AAV).
 CC The vectors comprise AAV inverted terminal repeats and constitutive or
 CC regulatable promoters for driving high levels of gene expression. Vectors
 CC encoding alpha-1-antitrypsin protein or a biologically active fragment or
 CC variant are administered to mammalian cells (preferably myofibers, or
 CC myoblasts, hepatocytes or lung cells) for treating alpha-1-antitrypsin
 CC deficiency or ameliorating a condition resulting from a defective
 CC protein. The vectors can also be useful for genetic therapy of other
 CC conditions such as hemophilia, adenosine deaminase deficiency, diabetes,
 CC cancer, autoimmune diseases, neurological disorders, immunodeficiency
 CC diseases and bacterial or viral infections by the infusion of protein or
 CC a cytokine such as interleukin-2

SQ Sequence 7492 BP; 1920 A; 1904 C; 1825 G; 1843 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 3; Length 7492;
 Best Local Similarity 100.0%; Pred. No. 3.8e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGGAC 60
 DB 27 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGGAC 86

QY 61 CTC 63
 DB 87 CTC 89

RESULT 33
 AAA59078
 ID AAA59078 standard; DNA; 8238 BP.
 XX
 AC AAA59078;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Nucleotide sequence of a plasmid.
 XX
 KW Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN WO200042208-A1.
 XX
 PD 20-JUL-2000.
 XX
 PF 14-JAN-2000; 2000WO-EP000265.
 XX
 PR 14-JAN-1999; 99US-0115920P.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GRS MEH.
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;
 PI Skripchenko Y;
 PI WPI; 2000-476068/41.
 DR
 XX
 PT New nucleic acid comprising an adenovirus tripartite leader nucleotide
 PT for producing high-capacity and targeted vectors for adenovirus-based
 PT gene therapy.
 XX
 PS Disclosure; Page 195-198; 212pp; English.
 XX
 CC The specification describes a nucleic acid molecule comprising an
 CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
 CC comprising two different TPL exons or three same or different TPL exons.
 CC The nucleic acid is used to produce an adenovirus vector particle,
 CC deliver an exogenous gene to a target cell, pseudotype recombinant viral
 CC vectors, target an adenovirus vector to a cell, produce a modified
 CC adenovirus, deliver a heterologous gene to an animal and produce a
 CC gutless adenoviral vector particle. The present sequence represents a
 CC plasmid, which is used in the course of the invention
 XX
 SQ Sequence 8238 BP; 1762 A; 2156 C; 2340 G; 1980 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 3; Length 8238;
 Best Local Similarity 100.0%; Pred. No. 3.8e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCACTGTTGTGCAC 60
 DB 742 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCACTGTTGTGCAC 801
 QY 61 CTC 63
 DB 802 CTC 804

RESULT 34
 AAT84562
 ID AAT84562 standard; cDNA; 8591 BP.
 XX

AC AAT84562;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-DEC-1997 (first entry)
 XX
 DE Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW muten; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;
 KW cyclic.
 XX
 OS Homo; sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 PH Key Location/Qualifiers
 FT CDS 2393..3856
 FT /*tag= a
 XX
 PN US5652092-A.
 XX
 PD 29-JUL-1997.
 XX
 PF 05-JUN-1995; 95US-00462859.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI; 1997-392937/36.
 DR P-PSDB; AAW26394.
 XX
 PT Screening for compounds which reduce beta-amyloid protein formation -
 PT using cells which express a construct encoding a marker and an amyloid
 PT precursor muten derived from APP isoforms.
 XX
 PS Disclosure; Fig 8; 84pp; English.
 XX
 CC Plasmid pCLL621 (AAT84562), desposited in E. coli as ATCC 69406, codes
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26394), that has a 276-amino acid deletion of the native APP and
 CC carries a Substance P epitope marker on the N-terminal side of the beta-
 CC amyloid protein (BAP) domain. APP-REP 751 can be used in a claimed method
 CC for screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 3.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCACTGTTGTGCAC 60
 DB 5177 TTTAAGTCCTAGCTCGATACAAATAAGCGCATTTGACCATTCACCACTGTTGTGCAC 5236
 QY 61 CTC 63
 DB 5237 CTC 5239

RESULT 35

AAT84561
 ID AAT84561 standard; cDNA; 8591 BP.
 XX
 AC AAT84561;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-DEC-1997 (first entry)
 XX
 DE Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW mutin; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;
 KW cyclic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 2393..3871
 FT /*tag= a
 XX
 FN US5652092-A.
 PD 29-JUL-1997.
 XX
 XX 05-JUN-1995; 95US-00462859.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI; 1997-392937/36.
 DR P-PSDB; AAW26393.
 XX
 PT Screening for compounds which reduce beta-amyloid protein formation -
 PT using cells which express a construct encoding a marker and an amyloid
 PT precursor mutin derived from APP isoforms.
 XX
 PS Disclosure; Fig 7; 84pp; English.
 XX
 CC Plasmid pCLL602 (AAT84561), deposited in E. coli as ATCC 69405, codes
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26393), that has a 276-amino acid deletion of the native APP and
 CC carries Substance P and Met-enkephalin epitope markers placed,
 CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid
 CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for
 CC screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 3.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGCCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 DB 5177 TTTAAGTGCCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGGCAC 5236
 QY 61 CTC 63
 |||

Db 5237 CTC 5239
 RESULT 36
 AAT87083
 ID AAT87083 standard; cDNA; 8591 BP.
 XX
 AC AAT87083;
 XX
 DT 25-MAR-2003 (revised)
 DT 06-JAN-1998 (first entry)
 XX
 DE Plasmid pCLL602 encoding amyloid precursor protein APP-REP 751.
 XX
 KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
 KW mutin; secretase; Alzheimer's disease; human; APP-REP 751; pCLL602; ds;
 KW cyclic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 2393..3871
 FT /*tag= a
 XX
 FN US5656477-A.
 PD 12-AUG-1997.
 XX
 XX 20-SEP-1993; 93US-00123659.
 PR 01-MAY-1992; 92US-00877675.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI; 1997-414594/38.
 DR P-PSDB; AAW26509.
 XX
 PT Nucleic acid encoding amyloid precursor mutin(s) - comprising reporter
 PT gene and coding sequence, for identifying compounds which modify the
 PT activity of proteolytic enzymes which cleave APP.
 XX
 PS Disclosure; Fig 7; 84pp; English.
 XX
 CC Plasmid pCLL602 (AAT87083), deposited in E. coli as ATCC 69405, codes
 CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
 CC (see AAW26509), that has a 276-amino acid deletion of the native APP and
 CC carries Substance P and Met-enkephalin epitope markers placed,
 CC respectively, on the N-terminal and C-terminal sites of the beta-amyloid
 CC protein (BAP) domain. APP-REP 751 can be used in a claimed method for
 CC screening for a compound which reduces the formation of beta-amyloid
 CC protein, determined by measuring the amount of marker in a medium
 CC containing transfected cells. The method is used to detect compounds
 CC which inhibit the activity of proteolytic enzymes which cleave APP to
 CC generate BAP fragments. Such compounds can be used in the treatment of
 CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
 CC distinguishes the construct from endogenously expressed APP, and
 CC beneficially increases the resolution of APP-REP fragments resulting from
 CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
 CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 3.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGCCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 DB 5177 TTTAAGTGCCTAGCTCGATCAATAAAGCCATTGACCATTCACCATTTGGTGGCAC 5236

QY 61 CTC 63
DB 5237 CTC 5239

RESULT 37
AAT87084
ID AAT87084 standard; cDNA; 8591 BP.
XX AC AAT87084;
XX DT 25-MAR-2003 (revised)
XX DT 06-JAN-1998 (first entry)
XX DE Plasmid pCLL621 encoding amyloid precursor protein APP-REP 751.
XX KW Amyloid precursor protein; APP; beta-amyloid protein; BAP; substrate;
KW Kunitz; secretase; Alzheimer's disease; human; APP-REP 751; pCLL621; ds;
XX KW cyclic.
XX OS Homo sapiens.
XX OS Synthetic.
XX OS Chimeric.
XX FH Key Location/Qualifiers
XX FT CDS 2393..3856
XX FT /*tag= a
XX FN US5656477-A.
XX PD 12-AUG-1997.
XX PF 20-SEP-1993; 93US-00123659.
XX PR 01-MAY-1992; 92US-00877675.
XX PA (AMCY) AMERICAN CYANAMID CO.
XX PI Jacobsen JS, Vitek MP;
XX WPI; 1997-414594/38.
XX DR P-PSDB; AAW26510.
XX PT Nucleic acid encoding amyloid precursor muten(s) - comprising reporter
XX PT gene and coding sequence, for identifying compounds which modify the
XX PT activity of proteolytic enzymes which cleave APP.
XX PS Disclosure; Fig 8; 84pp; English.
XX CC Plasmid pCLL621 (AAT87084), deposited in E. coli as ATCC 69406, codes
XX CC for an amyloid precursor protein (APP) substrate, designated APP-REP 751
XX CC (see AAW26510) that has a 276-amino acid deletion of the native APP and
XX CC carries a Substance P epitope marker on the N-terminal side of the beta-
XX CC amyloid protein (BAP) domain. APP-REP 751 can be used in a claimed method
XX CC for screening for a compound which reduces the formation of beta-amyloid
XX CC protein, determined by measuring the amount of marker in a medium
XX CC containing transfected cells. The method is used to detect compounds
XX CC which inhibit the activity of proteolytic enzymes which cleave APP to
XX CC generate BAP fragments. Such compounds can be used in the treatment of
XX CC e.g. Alzheimer's disease. The deletion of a 276 amino acid portion of APP
XX CC distinguishes the construct from endogenously expressed APP, and
XX CC beneficially increases the resolution of APP-REP fragments resulting from
XX CC the proteolytic cleavage by secretase or other amyloidogenic, BAP-
XX CC generating cleavage events. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGCTGATACATTAACGCCATTGACCATTCACACATTGGTGTGCAC 5236

DB 5177 TTTAAGTCCTAGCTGATACATTAACGCCATTGACCATTCACACATTGGTGTGCAC 5236
QY 61 CTC 63
DB 5237 CTC 5239

RESULT 38
AAV04866
ID AAV04866 standard; DNA; 8591 BP.
XX AC AAV04866;
XX DT 01-MAY-1998 (first entry)
XX DE cDNA encoding amyloid precursor protein mutant APP-ARP 751.
XX KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
KW amyloid precursor protein; APP; secretase; BAP aggregation;
XX KW abnormal proteolytic cleavage; ds.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 2393..3856
XX FT /*tag= a
XX FN US5703209-A.
XX PD 30-DEC-1997.
XX PF 05-JUN-1995; 95US-00464248.
XX PR 01-MAY-1992; 92US-00877675.
XX PR 20-SEP-1993; 93US-00123659.
XX PA (AMCY) AMERICAN CYANAMID CO.
XX PI Jacobsen JS, Vitek MP;
XX WPI; 1998-076482/07.
XX DR P-PSDB; AAW42979.
XX PT Amyloid precursor protein fusion polypeptides - comprising APP fragment
XX PT and marker, useful for research and drug screening.
XX PS Disclosure; Fig 8A-Q; 84pp; English.
XX CC The present sequence encodes an amyloid precursor protein (APP), which
XX CC has a deletion of 276 amino acids to within 15 amino acids of the beta-
XX CC amyloid peptide (BAP) domain. The protein also contains the abnormal
XX CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
XX CC is characteristic in brains of individuals suffering from Alzheimers
XX CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
XX CC protein which is derived from a larger amyloid precursor protein (APP).
XX CC APP is expressed as an integral membrane protein, and is cleaved by
XX CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
XX CC amyloidogenesis and results in the release of the amino-terminal APP
XX CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-
XX CC 770. These isoforms are derived by alternative splicing. APP-REP 751 is
XX CC constructed by ligating restriction fragments representing N- and C-
XX CC terminal APP-751 cDNA and substrate P reporter epitope sequences. APP
XX CC can be used as a substrate for studying abnormal proteolytic cleavage
XX CC which results in the release of BAP, and also to screen for drugs that
XX CC will inhibit such cleavage
XX SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACAATAAAGCCGATTTGACCATTCACCATTTGGTGGTGCAC 60
 |||||
 Db 5177 TTTAAGTGGCTAGCTCGATACAATAAAGCCGATTTGACCATTCACCATTTGGTGGTGCAC 5236

QY 61 CTC 63
 |||||
 Db 5237 CTC 5239

RESULT 39
 AAV04865
 ID AAV04865 standard; DNA; 8591 BP.
 XX
 AC AAV04865;
 XX
 DT 01-MAY-1998 (first entry)
 XX
 DE cDNA encoding amyloid precursor protein mutant APP-APP 751.
 XX
 KW Beta-amyloid peptide; BAP; extracellular BAP plaque;
 KW cerebrovascular deposit; Alzheimer's disease; Down's syndrome;
 KW amyloid precursor protein; APP; secretase; BAP aggregation;
 KW abnormal proteolytic cleavage; ds.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 2393..3871
 FT /*tag= a
 XX
 PN US5703209-A.
 XX
 PD 30-DEC-1997.
 XX
 XX 05-JUN-1995; 95US-00464248.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 PA
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI; 1998-076482/07.
 DR P-PSDB; AAW42978.
 XX
 PT Amyloid precursor protein fusion polypeptides - comprising APP fragment
 PT and marker, useful for research and drug screening.
 XX
 PS Disclosure; Fig 7A-Q; 84pp; English.
 XX
 CC The present sequence encodes an amyloid precursor protein (APP), which
 CC has a deletion of 276 amino acids to within 15 amino acids of the beta-
 CC amyloid peptide (BAP) domain. The protein also contains the Met-
 CC enkephalin reporter epitope at the carboxy terminus. Abnormal
 CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
 CC is characteristic in brains of individuals suffering from Alzheimers
 CC disease and Down's syndrome. BAP is a poorly soluble, self-aggregating
 CC protein which is derived from a larger amyloid precursor protein (APP).
 CC APP is expressed as an integral membrane protein, and is cleaved by
 CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
 CC amyloidogenesis and results in the release of the amino-terminal APP
 CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and APP-
 CC 770. These isoforms are derived by alternative splicing. APP-RP 751 is
 CC constructed by ligating restriction fragments representing N- and C-
 CC terminal APP-751 cDNA and substrate P reporter epitope sequences. APP
 CC can be used as a substrate for studying abnormal proteolytic cleavage
 CC which results in the release of BAP, and also to screen for drugs that
 CC will inhibit such cleavage

Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 2; Length 8591;
 Best Local Similarity 100.0%; Pred. No. 3.9e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACAATAAAGCCGATTTGACCATTCACCATTTGGTGGTGCAC 60
 |||||
 Db 5177 TTTAAGTGGCTAGCTCGATACAATAAAGCCGATTTGACCATTCACCATTTGGTGGTGCAC 5236

QY 61 CTC 63
 |||||
 Db 5237 CTC 5239

RESULT 40
 AAV05850
 ID AAV05850 standard; cDNA; 8591 BP.
 XX
 AC AAV05850;
 XX
 DT 01-JUN-1998 (first entry)
 XX
 DE APP-RP 751 gene from pCLL621.
 XX
 KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
 KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
 KW Alzheimer's disease; cleavage; cyclic; circular; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 2393..3856
 FT /*tag= a
 FT /product= "APP_REP_751"
 XX
 XX US5693478-A.
 XX
 PD 02-DEC-1997.
 XX
 XX 05-JUN-1995; 95US-00464247.
 XX
 PR 01-MAY-1992; 92US-00877675.
 PR 20-SEP-1993; 93US-00123659.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 PA
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI; 1998-031744/03.
 DR P-PSDB; AAW44745.
 XX
 PT Amyloid precursor mutin reporter molecule assay containing antibody
 PT recognised marker - used to study pathways associated with Alzheimer's
 FT disease.
 XX
 PS Disclosure; Fig 8; 84pp; English.
 XX
 CC This is the nucleotide sequence encoding a novel amyloid precursor
 CC protein (APP) designated APP-RP 751, contained in construct pCLL621. The
 CC sequence encodes a mutant version of the APP 751 isoform of human APP
 CC which contains a deletion of 276 amino acids from the central region. The
 CC deleted region is replaced by a substrate P reporter epitope sequence
 CC (RPKPQFFFGIM). In contrast to the APP-RP 751 encoded by the construct
 CC pCLL602 (AAV05849), this sequence does not contain a Met-enkephalin
 CC reporter epitope (YGGFM) fused at the C-terminus of the coding sequence.
 CC The shorter protein is generated for ease of detection based on size
 CC difference with the wild type APP protein and also by detection of the
 CC reporter epitopes. The mutant protein can be used in a method to study
 CC secretase and beta-amyloid protein (BAP)-generating pathways associated
 CC with Alzheimer's disease by studying proteolytic cleavage of the reporter
 CC polypeptides

SQ Sequence 8591 BP; 2225 A; 2038 C; 2248 G; 2080 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACAAATAAGCGCCATTGACCATTCACCATTCACCATTCGTTGTGCAC 60
DB 5177 TTTAAGTCCCTAGCTCGATACAAATAAGCGCCATTGACCATTCACCATTCACCATTCGTTGTGCAC 5236

QY 61 CTC 63
DB 5237 CTC 5239

RESULT 41
AAV05849
ID AAV05849 standard; cDNA; 8591 BP.
XX
AC AAV05849;
XX
DT 01-JUN-1998 (first entry)
XX
DE APP-REP 751 gene from pCLL602.
XX
KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
KW Alzheimer's disease; cleavage; cyclic; circular; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PH Key Location/Qualifiers
FT CDS 2393..3871
FT /tag= a
FT /product= "APP-REP_751"
XX
PN US5693478-A.
XX
PD 02-DEC-1997.
XX
PF 05-JUN-1995; 95US-00464247.
XX
PR 01-MAY-1992; 92US-00877675.
PR 20-SEP-1993; 93US-00123659.
XX
PA (ANCY) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek WP;
XX
PS WPI; 1998-031744/03.
XX
PT P-PSDB; AAW44744.
XX
FT Amyloid precursor muten reporter molecule assay containing antibody
FT recognised marker - used to study pathways associated with Alzheimer's
FT disease.
XX
PS Disclosure; Fig 7; 84pp; English.
XX
CC This is the nucleotide sequence encoding a novel amyloid precursor
CC protein (APP) designated APP-REP 751, contained in construct pCLL602. The
CC sequence encodes a mutant version of the APP 751 isoform of human APP
CC which contains a deletion of 276 amino acids from the central region. The
CC deleted region is replaced by a substrate P reporter epitope sequence
CC (RPKQPFGLM) and a Met-enkephalin reporter epitope (YGGFW) is fused at
CC the C-terminus. The shorter protein is generated for ease of detection
CC based on size difference with the wild type APP protein and also by
CC detection of the reporter epitopes. The mutant protein can be used in a
CC method to study secretase and beta-amyloid protein (BAP)-generating
CC pathways associated with Alzheimer's disease by studying proteolytic
CC cleavage of the reporter polypeptides
XX
SQ Sequence 8591 BP; 2225 A; 2038 C; 2247 G; 2081 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 2; Length 8591;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACAAATAAGCGCCATTGACCATTCACCATTCACCATTCGTTGTGCAC 60
DB 5177 TTTAAGTCCCTAGCTCGATACAAATAAGCGCCATTGACCATTCACCATTCACCATTCGTTGTGCAC 5236

QY 61 CTC 63
DB 5237 CTC 5239

RESULT 42
ABL57333
ID ABL57333 standard; DNA; 8902 BP.
XX
AC ABL57333;
XX
DT 29-AUG-2003 (revised)
DT 09-AUG-2002 (first entry)
XX
DE Vector plasmid PRIG-MP1.
XX
KW Vector; PRIG-MP1; promoter; ds.
XX
OS Cytomagalovirus.
OS Escherichia coli.
OS Rhesus macaque polyoma virus.
OS Rous sarcoma virus.
OS Chimeric.
XX
PN US2002055172-A1.
XX
PD 09-MAY-2002.
XX
PF 05-DEC-2000; 2000US-00729416.
XX
PR 07-OCT-1999; 99US-00414369.
XX
PA (HARR/) HARRINGTON J J.
XX
PI Harrington JJ;
XX
PS WPI; 2002-425568/45.
XX
FT Nucleic acid construct, for producing an expression product, comprises
FT two units each with a promoter sequence operably linked to an exon and
FT unpaired splice donor site.
XX
PS Disclosure; Page 23-27; 43pp; English.
XX
CC The present sequence is the nucleotide sequence of vector plasmid PRIG-
CC MP1. This plasmid includes 3 promoter/activation exon units, each
CC followed by a splice donor sequence, where the promoter is a
CC cytomegalovirus promoter and the activation exons do not encode a
CC translation start codon. A BamHI site is present downstream of the
CC promoter/exon units, and can be used to linearise the vector or to clone
CC a gene of interest into the vector. A neomycin-resistance selectable
CC marker gene under the control of a rous sarcoma virus is also present, as
CC well as a dihydrofolate reductase amplifiable marker under the control of
CC an SV40 promoter. A pUC plasmid origin of replication and a beta-
CC lactamase antibiotic resistance gene are also contained within PRIG-MP1.
CC The invention relates to improved methods for gene expression using
CC vectors with multiple promoters. A desired nucleic acid sequence is
CC introduced into the vector by conventional cloning or is expressed from
CC an endogenous sequence in the genome that is activated by the vector. The
CC vectors can be used to express cDNA clones, genomic DNA, chemically
CC synthesised nucleic acid molecules, antisense nucleic acids and
CC ribozymes, and also to activate endogenous genes in situ by homologous or
CC non-homologous recombination. The vectors may be transposon or retroviral
CC vectors. They can also be used to modify a gene of interest, and to

CC express a gene as a full-length or truncated protein. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 8902 BP; 2182 A; 2185 C; 2172 G; 2363 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 6; Length 8902;

Best Local Similarity 100.0%; Pred. No. 3.9e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACTGGTGTGCAC 60

DB 3826 TTTAAGTCCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACTGGTGTGCAC 3885

QY 61 CTC 63

DB 3886 CTC 3888

RESULT 43

AAA53873

ID AAA53873 standard; DNA; 9725 BP.

XX

AC AAA53873;

XX

DT 03-JAN-2001 (first entry)

XX

DE Expression vector pRIG19.

XX

KW Vector; endogenous gene; activation; over-expression; erythropoietin;

KW growth hormone; drug discovery; granulocyte colony stimulating factor;

KW ds.

XX

OS Synthetic.

XX

FN WO2000049162-A2.

XX

PD 24-AUG-2000.

XX

PF 22-FEB-2000; 2000WO-US004429.

XX

PR 19-FEB-1999; 99US-00253022.

PR 08-MAR-1999; 99US-00263814.

PR 26-MAR-1999; 99US-00276820.

XX

PA (ATHE-) ATHERSYS INC.

XX

PI Harrington JJ, Sherf B, Rundlett S;

XX

DR WPI; 2000-549276/50.

XX

PT Non-targeted activation of endogenous genes, e.g. for the production of erythropoietin, growth hormone or granulocyte-colony stimulating factor proteins and for drug discovery.

XX

PS Disclosure; Fig 30; 240pp; English.

XX

CC New methods, vectors and cells are described for non-targeted activation and over-expression of endogenous genes. The vector constructs comprise transcripational regulatory sequences (TRS) and unpaired splice donor sequences (USDS), preferably the vectors comprise (in sequential order) a TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization site (LS) with a second TRS linked to a selectable marker (SM) lacking a polyadenylation signal. The methods, vectors and cells comprising the CC vectors may be used for the non-targeted activation and over-expression of endogenous genes, e.g. for the production of proteins (including erythropoietin, growth hormone or granulocyte-colony stimulating factor) CC and drug discovery. The advantage of these methods are that endogenous CC genes including those associated with human disease and development, may CC be activated and isolated without prior knowledge of the sequence CC structure, function or expression profile of the genes being known

XX

Sequence 9725 BP; 2425 A; 2507 C; 2448 G; 2343 T; 0 U; 2 Other;

Query Match 100.0%; Score 63; DB 3; Length 9725;

Best Local Similarity 100.0%; Pred. No. 4e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACTGGTGTGCAC 60

DB 1610 TTTAAGTCCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACTGGTGTGCAC 1669

QY 61 CTC 63

DB 1670 CTC 1672

RESULT 44

AAA53879

ID AAA53879 standard; DNA; 9732 BP.

XX

AC AAA53879;

XX

DT 03-JAN-2001 (first entry)

XX

DE Expression vector pRIG-TP.

XX

KW Vector; endogenous gene; activation; over-expression; erythropoietin;

KW growth hormone; drug discovery; granulocyte colony stimulating factor;

KW ds.

XX

OS Synthetic.

XX

FN WO2000049162-A2.

XX

PD 24-AUG-2000.

XX

PF 22-FEB-2000; 2000WO-US004429.

XX

PR 19-FEB-1999; 99US-00253022.

PR 08-MAR-1999; 99US-00263814.

PR 26-MAR-1999; 99US-00276820.

XX

PA (ATHE-) ATHERSYS INC.

XX

PI Harrington JJ, Sherf B, Rundlett S;

XX

DR WPI; 2000-549276/50.

XX

PT Non-targeted activation of endogenous genes, e.g. for the production of erythropoietin, growth hormone or granulocyte-colony stimulating factor proteins and for drug discovery.

XX

PS Example 15; Fig 37; 240pp; English.

XX

CC New methods, vectors and cells are described for non-targeted activation and over-expression of endogenous genes. The vector constructs comprise transcripational regulatory sequences (TRS) and unpaired splice donor sequences (USDS), preferably the vectors comprise (in sequential order) a TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization site (LS) with a second TRS linked to a selectable marker (SM) lacking a polyadenylation signal. The methods, vectors and cells comprising the CC vectors may be used for the non-targeted activation and over-expression of endogenous genes, e.g. for the production of proteins (including erythropoietin, growth hormone or granulocyte-colony stimulating factor) CC and drug discovery. The advantage of these methods are that endogenous CC genes including those associated with human disease and development, may CC be activated and isolated without prior knowledge of the sequence CC structure, function or expression profile of the genes being known

XX

Sequence 9732 BP; 2427 A; 2512 C; 2443 G; 2348 T; 0 U; 2 Other;

Query Match 100.0%; Score 63; DB 3; Length 9732;

Best Local Similarity 100.0%; Pred. No. 4e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCCTAGCTCGATACAAATAAAGCGCATTTGACCATTCACCACTGGTGTGCAC 60

Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 1672
 QY 61 CTC 63
 Db 1673 CTC 1675

RESULT 45
 ID AAA53874
 AC AAA53874;
 DT 03-JAN-2001 (first entry)
 DE Expression vector pRIG20.
 KW Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 OS Synthetic.
 PN WO200049162-A2.
 PD 24-AUG-2000.
 PF 22-FEB-2000; 2000WO-US004429.
 PR 19-FEB-1999; 99US-00253022.
 PR 08-MAR-1999; 99US-00263814.
 PR 26-MAR-1999; 99US-00276820.
 XX (ATHE-) ATHERSYS INC.
 XX Harrington JJ, Sherf B, Rundlett S;
 XX WPI; 2000-549276/50.
 XX Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.
 XX Disclosure; Fig 31; 240pp; English.
 XX New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known
 XX Sequence 9738 BP; 2428 A; 2514 C; 2447 G; 2347 T; 0 U; 2 Other;
 SQ Query Match 100.0%; Score 63; DB 3; Length 9738;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 60
 Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 1672
 QY 61 CTC 63

Db 1673 CTC 1675

RESULT 46
 ID AAA53875
 AC AAA53875;
 DT 03-JAN-2001 (first entry)
 DE Expression vector pRIGadl.
 KW Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 OS Synthetic.
 PN WO200049162-A2.
 PD 24-AUG-2000.
 PF 22-FEB-2000; 2000WO-US004429.
 PR 19-FEB-1999; 99US-00253022.
 PR 08-MAR-1999; 99US-00263814.
 PR 26-MAR-1999; 99US-00276820.
 XX (ATHE-) ATHERSYS INC.
 XX Harrington JJ, Sherf B, Rundlett S;
 XX WPI; 2000-549276/50.
 XX Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.
 XX Disclosure; Fig 32; 240pp; English.
 XX New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, an USDS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known
 XX Sequence 9873 BP; 2450 A; 2557 C; 2501 G; 2363 T; 0 U; 2 Other;
 SQ Query Match 100.0%; Score 63; DB 3; Length 9873;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 60
 Db 1752 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 1811
 QY 61 CTC 63
 Db 1812 CTC 1814

RESULT 47
 ID AAA53876

ID AA53876 standard; DNA; 10054 BP.
 AC AA53876;
 XX
 DT 03-JAN-2001 (first entry)
 XX
 DE Expression vector pRIGbdl.
 XX
 XX Vector; endogenous gene; activation; over-expression; erythropoietin;
 KW growth hormone; drug discovery; granulocyte colony stimulating factor;
 KW ds.
 XX
 OS Synthetic.
 XX
 FN WC200049162-A2.
 XX
 PD 24-AUG-2000.
 XX
 PF 22-FEB-2000; 2000WO-US004429.
 XX
 PR 19-FEB-1999; 99US-00253022.
 PR 08-MAR-1999; 99US-00263814.
 PR 26-MAR-1999; 99US-00276820.
 XX
 PA (ATHE-) ATHERSYS INC.
 XX
 PI Harrington JJ, Sherf B, Rundlett S;
 XX
 DR WPI; 2000-549276/50.
 XX
 PT Non-targeted activation of endogenous genes, e.g. for the production of
 PT erythropoietin, growth hormone or granulocyte-colony stimulating factor
 PT proteins and for drug discovery.
 XX
 XX Disclosure; Fig 33; 240pp; English.
 XX
 CC New methods, vectors and cells are described for non-targeted activation
 CC and over-expression of endogenous genes. The vector constructs comprise
 CC transcriptional regulatory sequences (TRS) and unpaired splice donor
 CC sequences (USDS), preferably the vectors comprise (in sequential order) a
 CC TRS, a rare cutting restriction site (RCRS) and a linearization
 CC site (LS) with a second TRS linked to a selectable marker (SM) lacking a
 CC polyadenylation signal. The methods, vectors and cells comprising the
 CC vectors may be used for the non-targeted activation and over-expression
 CC of endogenous genes, e.g. for the production of proteins (including
 CC erythropoietin, growth hormone or granulocyte-colony stimulating factor)
 CC and drug discovery. The advantage of these methods are that endogenous
 CC genes including those associated with human disease and development, may
 CC be activated and isolated without prior knowledge of the sequence
 CC structure, function or expression profile of the genes being known
 XX
 SQ Sequence 10054 BP; 2548 A; 2562 C; 2515 G; 2427 T; 0 U; 2 Other;
 Query Match 100.0%; Score 63; DB 3; Length 10054;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTTGGTGAC 60
 DB 1935 TTTAAGTGGCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTTGGTGAC 1994
 QY 61 CTC 63
 DB 1995 CTC 1997
 RESULT 48
 ID AA59501 standard; DNA; 11265 BP.
 XX
 AC AA59501;
 XX
 DT 17-OCT-2003 (revised)

DT 02-FEB-1999 (first entry)
 XX
 DE Plasmid pREP7::CTLA4-hlg.
 XX
 KW pREP7::CTLA4-hlg; plasmid; CTLA4; immunoglobulin; vaccine;
 KW DNA immunisation; human; mouse; ds; circular; cyclic.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 FN WC9844129-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 26-MAR-1998; 98WO-AU000208.
 XX
 PR 27-MAR-1997; 97AU-00005891.
 PR 13-FEB-1998; 98AU-00001830.
 XX
 XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UTME) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (CSLC-) CSL LTD.
 XX
 XX Boyle JS, Brady JL, Lew AM;
 FI
 XX
 DR WPI; 1998-557122/47.
 XX
 PT DNA molecule for raising an immune response to antigen - comprises
 PT sequence encoding dimerisation or multimerisation polypeptide.
 XX
 PS Disclosure; Page 32-37; 64pp; English.
 XX
 CC This is the DNA sequence of expression plasmid pREP7::CTLA4-hlg that
 CC encodes a secreted form of the Fc fragment of human IgG1 fused to murine
 CC CTLA4. The invention provides a new DNA molecule for use in raising an
 CC immune response to an antigen. The DNA molecule comprises: (i) a first
 CC sequence encoding a targeting molecule (e.g. CTLA4, which acts as a
 CC targeting molecule to antigen-presenting cells expressing B-7); (ii) a
 CC second sequence encoding the antigen or its epitope, and (iii) optionally
 CC a third sequence encoding a polypeptide (e.g. an immunoglobulin) which
 CC promotes dimerisation or multimerisation of the product encoded by the
 CC DNA molecule. Also claimed are a polypeptide encoded by the DNA molecule,
 CC and a vector including the DNA molecule. The inventors have shown that
 CC fusion proteins consisting of antigen and cell surface receptor ligands
 CC can deliver antigen to sites of immune induction which enhance the immune
 CC response and possibly the efficacy of genetic vaccines. The DNA molecule
 CC can be used in a claimed method for deviating an immune response to an
 CC antigen in an individual. (Updated on 17-OCT-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 11265 BP; 2717 A; 2979 C; 3002 G; 2567 T; 0 U; 0 Other;
 Query Match 100.0%; Score 63; DB 2; Length 11265;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTTGGTGAC 60
 DB 571 TTTAAGTGGCTAGCTCGATACATAAAGCCATTTCACCATTCACCATTTGGTGAC 630
 QY 61 CTC 63
 DB 631 CTC 633
 RESULT 49
 ID AA59077 standard; DNA; 11600 BP.
 XX
 AC AA59077;

XX 07-NOV-2000 (first entry)
XX Nucleotide sequence of plasmid pMNeoE2a-3.1.
XX Adenovirus; tripartite leader; adenovirus vector particle; gene delivery;
KW ss.
XX Synthetic.
XX WO200042208-A1.
XX 20-JUL-2000.
XX 14-JAN-2000; 2000WO-EP000265.
XX 14-JAN-1999; 99US-0115920P.
XX (NOVS) NOVARTIS AG.
XX (SCRI) NOVARTIS-ERFINDUNGEN VERW GES MEH.
XX (SCRI) SCRIPPS RES INST.
XX Nemerow GR, Von Seggern DJ, Hallenbeck PL, Stevenson SC;
PI Skripchenko Y;
XX WPI; 2000-476068/41.
XX New nucleic acid comprising an adenovirus tripartite leader nucleotide
PT for producing high-capacity and targeted vectors for adenovirus-based
PT gene therapy.
XX Example 6; Page 192-195; 212pp; English.
XX The specification describes a nucleic acid molecule comprising an
CC adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence
CC comprising two different TPL exons or three same or different TPL exons.
CC The nucleic acid is used to produce an adenovirus vector particle,
CC deliver an exogenous gene to a target cell, pseudotype recombinant viral
CC vectors, target an adenovirus vector to a cell, produce a modified
CC adenovirus, deliver a heterologous gene to an animal and produce a
CC plasmid adenoviral vector particle. The present sequence represents
CC plasmid pMNeoE2a-3.1, which is used in the course of the invention
XX
SQ Sequence 11600 BP; 2929 A; 2747 C; 3012 G; 2912 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 3; Length 11600;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCTAGCTCGATACATATAACGCCATTGGACCATTCACCATTTGGTGTCAC 60
DB 27 TTTAAGTGCTAGCTCGATACATATAACGCCATTGGACCATTCACCATTTGGTGTCAC 86
QY 61 CTC 63
DB 87 CTC 89
RESULT 50
ABA94279
ID ABA94279 standard; DNA; 11600 BP.
XX ABA94279;
XX ABA94279;
XX 13-MAR-2002 (first entry)
XX Nucleotide sequence of plasmid MMTV-E2a-SV40-Neo.
XX Adenovirus; inverter terminal repeat sequence; ITRS; ocular disease;
KW fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STDG1;
KW opthalmological; antiinflammatory; antidiabetic; cytostatic;
KW gene therapy; tripartite leader; TPL; ss.
XX

OS Synthetic.
XX WO200183729-A2.
XX 08-NOV-2001.
XX 30-APR-2001; 2001WO-EP004863.
XX 01-MAY-2000; 2000US-00562934.
XX (NOVS) NOVARTIS AG.
XX (SCRI) SCRIPPS RES INST.
XX (NEME/) NEMEROW G R.
XX (VSEG/) VON SEGGERN D J.
XX (FRIE/) FRIEDLANDER M.
XX Nemerow GR, Von Seggern DJ, Friedlander M;
XX WPI; 2002-082846/11.
XX Polynucleotide for making vectors, useful for treating ocular diseases,
PT e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat
PT sequences, packaging signal and photoreceptor-specific promoter.
XX Example 5; Page 141-145; 149pp; English.
XX The invention provides an isolated polynucleotide comprising adenovirus
CC (AV) inverter terminal repeat sequences (ITRS), AV packaging signal
CC operatively linked to ITRS and a photoreceptor-specific promoter. A
CC recombinant AV vector (AVV) comprising the polynucleotide is useful for
CC targeted delivery of a gene product to the eye (especially to the
CC vitreous cavity), for treating an ocular disease, e.g., retinal
CC degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic
CC retinopathies, retinal vascularizations, and retinoblastoma, of a mammal
CC preferably human. The AAV comprises a fiber protein that specifically or
CC selectively binds to receptors that are expressed on cells (preferably
CC photoreceptors in the eye). Preferably, the recombinant virus comprise a
CC fiber protein from an adenovirus type D subgroup or is a chimeric protein
CC containing a portion of the N-terminus of an adenovirus type 2 or type 5
CC penton, and the therapeutic product is a trophic factor, an anti-
CC apoptotic factor, gene encoding a rhodopsin protein, a wild-type
CC stargardt disease gene (STDG1), an anti-cancer agent and a protein that
CC regulates expression of a photoreceptor specific gene product. The viral
CC nucleic acid of AAV comprises ITRS and packaging signal derived from AAV
CC subgroup B or C, especially an AV type 2 or type 5. AAV is also useful
CC for targeted gene therapy, where the vector comprises an AV type 37 fiber
CC protein or its portion, and selectively transduces photoreceptors and
CC delivers a gene product encoded by AAV. The present sequence represents
CC the nucleotide sequence of plasmid MMTV-E2a-SV40-Neo
XX
SQ Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 6; Length 11600;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCTAGCTCGATACATATAACGCCATTGGACCATTCACCATTTGGTGTCAC 60
DB 27 TTTAAGTGCTAGCTCGATACATATAACGCCATTGGACCATTCACCATTTGGTGTCAC 86
QY 61 CTC 63
DB 87 CTC 89
RESULT 51
AAL56865
ID AAL56865 standard; DNA; 11600 BP.
XX AAL56865;
XX AAL56865;
XX 06-NOV-2003 (first entry)
XX

DE DNA sequence of the plasmid MMTV-E2a-SV40-Neo construct.

XX Fibre shaft modification; adenoviral vector; cell entry pathway; penton;

KW CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;

KW gene therapy; fibre knob; ds.

XX Rhesus macaque polyoma virus.

OS Unidentified adenovirus.

OS Unidentified.

XX WO2003062400-A2.

PN 31-JUL-2003.

XX 24-JAN-2003; 2003WO-US002295.

XX 24-JAN-2002; 2002US-0350388P.

PR 26-JUN-2002; 2002US-0391967P.

XX (SCRI) SCRIPPS RES INST.

PA (NOVS) NOVARTIS AG.

XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;

PI WPI; 2003-627459/59.

XX New modified adenovirus capsid protein, useful as a base vector for

PT producing redirected adenoviruses.

XX Disclosure; Page 143-146; 132pp; English.

XX This invention relates to novel fibre shaft modifications in adenoviral

CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a

CC specific targeted tissue or organ, accordingly gene therapy requires the

CC ablation of normal virus tropism. If successful, systemic vector delivery

CC into a peripheral vein would be targeted to the desired location in the

CC body without any associated side effects, which would permit lower, less

CC toxic vector doses that are also potentially less immunogenic. The

CC present invention describes capsid modifications, specifically fibre

CC shaft mutations that when expressed on adenoviral particles ablates

CC binding to heparin sulphate proteoglycans (HSP) thus providing detargeted

CC vectors. Furthermore, when this is combined with modifications of other

CC adenoviral proteins involved in the cell entry pathway such as the fibre

CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors

CC become fully detargeted. As such, these fully ablated particles can be

CC used in vivo as base vectors for producing redirected adenoviruses with

CC the desired cell specificity. This polynucleotide sequence is the plasmid

CC MMTV-E2a-SV40-Neo construct used to provide complementation of the

CC adenoviral E2a function of the invention

XX

SQ Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 8; Length 11600;

Best local Similarity 100.0%; Pred. No. 4.2e-14;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTAACTGCTAGCTCGACATATTAAGCCATTTGACATTCACCATTTGCTGTGAC 60

DB 27 TTTTAACTGCTAGCTCGACATATTAAGCCATTTGACATTCACCATTTGCTGTGAC 86

QY 61 CTC 63

DB 87 CTC 89

RESULT 52

AD875125

ID AD875125 standard; DNA; 11600 BP.

AC AD875125;

XX 04-DEC-2003 (first entry)

XX

DE Chromosomal insertion pWNeO2a-3.1.

XX ophthalmological; antiinflammatory; antidiabetic; gene therapy;

KW adenovirus inverted terminal repeat sequence;

KW adenovirus packaging signal; photoreceptor-specific promoter;

KW adenovirus type 37; adenovirus type D serotype; adenovirus type 2;

KW rhodopsin; wild-type Stargardt disease gene; STGD1; anti-apoptotic factor;

KW retinal degenerative disease; retinitis pigmentosa; Stargardt's disease;

KW diabetic retinopathy; retinal vascularisation; chorioideraemia;

KW gyrate atrophy; macular dystrophy; retinoblastoma;

KW photoreceptor-restricted transgene expression;

KW recombinant adenovirus vector; adenovirus type 5; E2a;

KW chromosomal insertion; ds.

XX Homo sapiens.

OS US2002193327-A1.

PN 19-DEC-2002.

XX 01-MAY-2001; 2001US-00847101.

PF 01-MAY-2000; 2000US-00562934.

PR (SCRI) SCRIPPS RES INST.

XX Nemerow GR, Von Seggern DJ, Friedlander M;

PI WPI; 2003-657234/62.

XX Novel nucleic acids comprising adenovirus inverted terminal repeat

PT sequences, adenovirus packaging signals operatively linked to the

PT sequences and photoreceptor-specific promoters, useful for treating

PT retinitis pigmentosa.

XX Example 5; Page 93-98; 106pp; English.

XX The invention describes an isolated nucleic acid (I) comprising

CC adenovirus inverted terminal repeat sequence, an adenovirus packaging

CC signal operatively linked to the sequence, and a photoreceptor-specific

CC promoter. A Recombinant adenovirus vector (II) comprising (I) is useful

CC for targeted delivery of a gene product to the eye of a mammal which

CC involves administering (II) that comprises heterologous DNA encoding the

CC gene product or resulting in expression of the gene product, where the

CC recombinant virus comprises a fibre protein that specifically or

CC selectively binds to receptors that are expressed on cells which are

CC photoreceptors, in the eye. The recombinant virus comprises a fibre

CC protein which is an adenovirus type 37, from an adenovirus type D

CC serotype. The fibre is a chimeric protein containing a sufficient portion

CC of the N-terminus of an adenovirus type 2 or type 5 fibre protein for

CC interaction with an adenovirus type 2 or type 5 penton, and a sufficient

CC portion of an adenovirus serotype D knob portion of the fiber for

CC selective binding to photoreceptors in the eye of a mammal. The

CC encapsulated nucleic acid comprises a photoreceptor-specific promoter

CC operatively linked to a nucleic acid comprising the therapeutic product

CC which is chosen from tropic factor, anti-apoptotic factor, gene encoding

CC a rhodopsin protein, wild-type Stargardt disease gene (STGD1), an anti-

CC cancer agent and a protein that regulates expression of a photoreceptor-

CC specific gene product. The delivery is effected for treatment of an

CC ocular disease such as retinal degenerative disease e.g., retinitis

CC pigmentosa, Stargardt's disease, diabetic retinopathies, retinal

CC vascularisation, chorioideraemia, gyrate atrophy or macular dystrophy or

CC retinoblastoma inherited and acquired retinal and neovascular

CC degenerative diseases. The viral nucleic acid comprises an adenovirus

CC inverted terminal repeat (ITR) sequences, and an adenovirus packaging

CC signal operatively linked to the sequence. The ITRs and packaging signal

CC are derived from an adenovirus serotype B or C, or adenovirus type 2 or

CC 5. The viral nucleic acid further comprises a photoreceptor-specific

CC promoter. (II) includes photoreceptor promoters providing a means not

CC only for specific targeting of expression in these cells, but also for

CC photoreceptor-restricted transgene expression. This sequence represents a

CC chromosomal insertion found in adenoviral plasmids of the A549 lung

CC carcinoma cell line which provide a complement of adenoviral E2a gene
CC function.
XX Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;
SQ Sequence 11600 BP; 2929 A; 2747 C; 3011 G; 2913 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 9; Length 11600;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGTTGTCAC 60
DB 27 TTTAAGTCCCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGTTGTCAC 86
QY 61 CTC 63
DB 87 CTC 89
RESULT 53
AAL55269
ID AAL55269 standard; DNA; 16958 BP.
XX AAL55269;
DT 10-MAY-2003 (first entry)
XX DNA of expression vector RC77, SEQ ID No 3.
DE Vector; excisable; site-specific recombinase; enzyme; exogenous;
KW signalling molecule; transcription factor; cell metabolism;
KW differentiation state; kinase; phosphatase; ds.
XX Unidentified.
XX WO2003002735-A2.
XX 09-JAN-2003.
XX 28-JUN-2002; 2002WO-CA000997.
XX 28-JUN-2001; 2001US-0301149P.
XX (PHEN-) PHENOGENE THERAPEUTICS INC.
XX Lanctot C, Gingras R, Gaumont M;
XX WPI; 2003-210275/20.
XX New vector having a nucleic acid sequence excisable by site-specific
XX recombination, useful for identifying or selecting exogenous nucleic
XX acids with desired features, e.g. nucleic acids encoding transcription
XX factors or kinases.
XX Claim 24; Page 103-112; 122pp; English.
XX The invention relates to novel vectors comprising nucleic acid sequences
XX excisable by a site-specific recombinase. The vectors or cells are useful
XX for identifying or selecting an exogenous nucleic acid having a desired
XX feature, e.g. nucleic acids encoding signalling molecules, transcription
XX factors or other proteins involved in changes of cell metabolism or
XX differentiation state (e.g. kinase or phosphatase). This polynucleotide
XX sequence represents the DNA of the vector RC77 relating to the invention
XX
SQ Sequence 16958 BP; 4816 A; 4210 C; 4125 G; 3807 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 7; Length 16958;
Best Local Similarity 100.0%; Pred. No. 4.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGTTGTCAC 60
DB 14710 TTTAAGTCCCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGTTGTCAC 14769

QY 61 CTC 63
DB 14770 CTC 14772
RESULT 54
AAL56867
ID AAL56867 standard; DNA; 33622 BP.
XX AAL56867;
DT 06-NOV-2003 (first entry)
XX DNA sequence of the recombinant adenoviral Av3nBg vector.
DE Fibre shaft modification; adenoviral vector; cell entry pathway; penton;
KW CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;
KW gene therapy; fibre knob; Av3nBg; ds.
XX Human adenovirus type 5.
XX Unidentified.
XX WO2003062400-A2.
XX 31-JUL-2003.
XX 24-JAN-2003; 2003WO-US002295.
XX 24-JAN-2002; 2002US-0350388P.
XX 26-JUN-2002; 2002US-0391967P.
XX (SCRI) SCRIPPS RES INST.
XX (NOVS) NOVARTIS AG.
XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;
XX WPI; 2003-627459/59.
XX New modified adenovirus capsid protein, useful as a base vector for
XX producing redirected adenoviruses.
XX Example 1; Page 156-165; 132pp; English.
XX This invention relates to novel fibre shaft modifications in adenoviral
XX vectors. Adenoviral vector-mediated gene therapy aims to transduce a
XX specific targeted tissue or organ, accordingly gene therapy requires the
XX ablation of normal virus tropism. If successful, systemic vector delivery
XX into a peripheral vein would be targeted to the desired location in the
XX body without any associated side effects, which would permit lower, less
XX toxic vector doses that are also potentially less immunogenic. The
XX present invention describes capsid modifications, specifically fibre
XX shaft mutations that when expressed on adenoviral particles ablates
XX binding to heparin sulphate proteoglycans (HSP) thus providing detargeted
XX vectors. Furthermore, when this is combined with modifications of other
XX adenoviral proteins involved in the cell entry pathway such as the fibre
XX knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors
XX become fully detargeted. As such, these fully ablated particles can be
XX used in vivo as base vectors for producing redirected adenoviruses with
XX the desired cell specificity. This polynucleotide sequence is the
XX recombinant E1, E2a and E3-deleted adenoviral vector (Av3nBg) that
XX encodes a nuclear localising beta-galactosidase, used in the
XX exemplification of the invention
XX
SQ Sequence 33622 BP; 7857 A; 9539 C; 9277 G; 6949 T; 0 U; 0 Other;
Query Match 100.0%; Score 63; DB 8; Length 33622;
Best Local Similarity 100.0%; Pred. No. 5.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGTTGTCAC 60
DB 734 TTTAAGTCCCTAGCTCGATACATAAAGCCCATTTGACCATTCACCATTTGTTGTCAC 793

QY 61 CTC 63
 DB 794 CTC 796

RESULT 55
 AAZ94163
 ID AAZ94163 standard; DNA; 34302 BP.
 XX AAZ94163;
 AC AAZ94163;
 XX 15-SEP-2003 (revised)
 DT 19-JUN-2000 (first entry)
 XX Adenovirus vector Ad5RSVp16 used for prostate cancer gene therapy.
 DE Ad5RSVp16; adenovirus; vector; RSV; promoter; human; p16;
 XX tumour suppressor gene; prostate cancer; gene therapy; ds.
 KW Human adenovirus type 5.
 OS Rous sarcoma virus.
 OS Homo sapiens.
 OS Chimeric.
 XX Key Location/Qualifiers
 FH promoter 410..805
 FT /*tag= a
 FT misc_feature 1055..2014
 FT /*tag= b
 FT /*note= "p16 sense cDNA"
 XX WO200014211-A1.
 XX 16-MAR-2000.
 XX 02-SEP-1999; 99WO-US018833.
 XX 02-SEP-1998; 98DS-00145729.
 XX (GENO-) GENOTHERAPEUTICS INC.
 XX Steiner WS, Lu Y;
 XX WPI; 2000-256967/22.
 XX Replication-deficient adenovirus type 5 expression vector, useful in gene
 PT therapy of prostate cancer, comprises a nucleic acid encoding p16 under
 PT the control of a Rous Sarcoma virus promoter.
 XX Disclosure; Fig 13; 118pp; English.
 XX The present sequence is that of replication-deficient adenovirus vector
 CC Ad5RSVp16, deposited as ATCC VR 2626. The vector is a type 5 adenovirus
 CC in which the E1 and E3 regions of the genome have been removed, and a p16
 CC tumour suppressor gene (see AAZ94162) has been inserted under control of
 CC a Rous sarcoma virus (RSV) promoter (see AAZ94161). Ad5RSVp16 can be used
 CC in the gene therapy of prostate cancer to replace a missing, mutated or
 CC inactivated p16 gene. In vitro, PC3 cells which were stably transfected
 CC with the vector showed a 70% reduction in cell number. The vector also
 CC inhibited growth of prostate cancer cells PPC-1, DU145 and PC3 in
 CC culture. PPC-1 tumours grown in nude mice treated by a single injection
 CC of Ad5RSVp16 had a marked reduction in tumour size when compared to
 CC untreated control. The mice also survived for longer. Transduction rates
 CC were over 90%, with transgene expression detectable in tumours for up to
 CC 2 wk. (Updated on 15-SEP-2003 to standardise OS field)
 XX Sequence 34302 BP; 7995 A; 9797 C; 9303 G; 7207 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 3; Length 34302;
 Best Local Similarity 100.0%; Pred. No. 5.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATCAATTAAGCCATTGACCATTTGACCATTTGCTGCAC 60

DB 742 TTTAAGTGCTAGCTCGATCAATTAAGCCATTGACCATTTGACCATTTGCTGCAC 801
 QY 61 CTC 63
 DB 802 CTC 804

RESULT 56
 AAL56866
 ID AAL56866 standard; DNA; 35211 BP.
 XX AAL56866;
 AC AAL56866;
 XX 06-NOV-2003 (first entry)
 DT DNA sequence of the recombinant adenoviral AvinBg vector.
 DE Fibre shaft modification; adenoviral vector; cell entry pathway; penton;
 XX CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP;
 KW gene therapy; fibre knob; AvinBg; ds.
 XX Human adenovirus type 5.
 OS Unidentified.
 OS WO2003062400-A2.
 XX 31-JUL-2003.
 XX 24-JAN-2003; 2003WO-US002295.
 XX 24-JAN-2002; 2002US-0350388P.
 PR 26-JUN-2002; 2002US-0391967P.
 XX (SCRI) SCRIPPS RES INST.
 PA (NOVS) NOVASTIS AG.
 XX Kaleko M, Nemerow GR, Smith T, Stevenson SC;
 XX WPI; 2003-627459/59.
 XX New modified adenovirus capsid protein, useful as a base vector for
 PT producing redirected adenoviruses.
 XX Example 1; Page 146-156; 132pp; English.
 CC This invention relates to novel fibre shaft modifications in adenoviral
 CC vectors. Adenoviral vector-mediated gene therapy aims to transduce a
 CC specific targeted tissue or organ, accordingly gene therapy requires the
 CC ablation of normal virus tropism. If successful, systemic vector delivery
 CC into a peripheral vein would be targeted to the desired location in the
 CC body without any associated side effects, which would permit lower, less
 CC toxic vector doses that are also potentially less immunogenic. The
 CC present invention describes capsid modifications, specifically fibre
 CC shaft mutations that when expressed on adenoviral particles ablates
 CC binding to heparin sulphate proteoglycans (HSP) thus providing detargeted
 CC vectors. Furthermore, when this is combined with modifications of other
 CC adenoviral proteins involved in the cell entry pathway such as the fibre
 CC knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors
 CC become fully detargeted. As such, these fully ablated particles can be
 CC used in vivo as base vectors for producing redirected adenoviruses with
 CC the desired cell specificity. This polynucleotide sequence is the
 CC recombinant E1 and E3-deleted adenoviral vector (AvinBg) that encodes a
 CC nuclear localising beta-galactosidase, used in the exemplification of the
 CC invention
 XX Sequence 35211 BP; 8136 A; 10028 C; 9704 G; 7343 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 8; Length 35211;
 Best Local Similarity 100.0%; Pred. No. 5.3e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATCAATTAAGCCATTGACCATTTGACCATTTGCTGCAC 60

Db 848 TTTAAGTCCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 907
QY 61 CTC 63
Db 908 CTC 910

RESULT 57
AA02780
ID AAX02780 standard; DNA; 37808 BP.
XX AC AAX02780;
XX 14-MAY-1999 (first entry)
XX Vector pMVX-BG DNA.
XX Vector pMVX-BG; cloning; adenoviral minimal virus; AdMV; ITR; plasmid;
KW inverted terminal repeats; ITR; packaging signal; PSI; bacteriophage;
KW virus bank; genomic analysis; transgenic animal; ss.
XX Synthetic.
XX WO9902647-A2.
XX 21-JAN-1999.
XX 06-JUL-1998; 98WO-DE001940.
XX 10-JUL-1997; 97DE-01029571.
PR 10-OCT-1997; 97DE-01044768.
XX (HEPA-) HEPAVEC GENTHERAPIE AG.
XX Hillgenberg M, Loeser P, Schmieders F, Sandig V, Strauss M;
PI WPI; 1999-120851/10.
XX New cloning vector for producing adenoviral minimal viruses - useful for
PT gene therapy or for preparation of virus banks and transgenic animals.
XX Disclosure; Page 16-41; 57pp; German.
XX This invention describes a novel cloning vector (A) for production of
CC adenoviral minimal viruses (AdMV). The vector is composed of two
CC adenoviral inverted terminal repeats (ITR) and a bacterial plasmid
CC backbone that includes an origin of replication (ori) and bacterial
CC resistance gene, in which a packaging signal (PS1) for a bacteriophage is
CC cloned. ITR are flanked by two cleavage sites for a restriction
CC endonuclease (RE) and they frame an adenoviral packaging signal (PS2), a
CC multiple cloning site for insertion of a therapeutic DNA (in which
CC optionally additional, non-coding chromosomal mammalian DNA is cloned),
CC optionally a recognition site for a recombinase (between the ITR and PS2)
CC and optionally a reporter gene cassette (RGS). AdMV produced from this
CC vector are useful for all adenoviral gene transfer applications, for
CC production of virus banks (e.g. for genomic analysis) and for preparation
CC of transgenic animals. AdMV are safe, compatible with all helper systems,
CC and can accommodate large DNA inserts (particularly complete genes with
CC the native chromosomal organisation, including the native promoter so
CC that problems of over-expression caused by viral promoters are avoided).
CC The use of PSI makes possible the use of very efficient and size
CC selecting cosmid cloning techniques. When used for transgenic animal
CC production, the AdMV can include long homologous regions to provide a
CC higher frequency of recombination
XX Sequence 37808 BP; 10910 A; 7906 C; 8561 G; 10423 T; 0 U; 8 Other;
SQ

Query Watch 100.0%; Score 63; DB 2; Length 37808;
Best Local Similarity 100.0%; Pred. No. 5.4e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60

Db 28950 TTTAAGTCCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 28409
QY 61 CTC 63
Db 28410 CTC 28412

RESULT 58
ABL59282
ID ABL59282 standard; DNA; 92 BP.
XX AC ABL59282;
XX 07-AUG-2003 (revised)
DT 07-OCT-2002 (first entry)
XX Nucleotide sequence of fragment 9190300 from LTR of ALSV.
XX Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
XX Avian leukosis virus.
XX US6391555-B1.
XX 21-MAY-2002.
XX 07-JAN-2000; 2000US-00479770.
XX 07-JAN-1999; 99US-0115087P.
XX (JOHN/) JOHNSON E S.
XX Johnson ES;
XX WPI; 2002-478534/51.
XX Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
PT long terminal repeats, in a DNA sample from a patient indicates that the
PT patient has, or is likely to develop ALSV-induced lung cancer.
XX Disclosure; Fig 8; 25pp; English.
XX ABL59276-86 represent PCR amplified fragments from a conserved region of
CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
CC ABL59283 represents a positive control from a chicken tumour induced by
CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
CC which the amplified sequence showed closest homology. The primers used
CC for amplification were used to screen for an increased potential for
CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
CC nucleic acid sequences in DNA from a sample from the patient. The method
CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
CC 2003 to correct OS field.)
XX Sequence 92 BP; 25 A; 21 C; 19 G; 27 T; 0 U; 0 Other;
SQ

Query Watch 98.4%; Score 62; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.4e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTCCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 27 TTTAAGTCCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 86

QY 61 CT 62
Db 87 CT 88

RESULT 59
ABL59283
ID ABL59283 standard; DNA; 178 BP.

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XX AC ABL59283;
XX DT 07-AUG-2003 (revised)
XX DT 07-OCT-2002 (first entry)
XX DE Nucleotide sequence of fragment 1L3B from LTR of ALSV.
XX KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
XX OS Avian leukosis virus.
XX PN US6391555-B1.
XX PD 21-MAY-2002.
XX PF 07-JAN-2000; 2000US-00479770.
XX PR 07-JAN-1999; 99US-0115087P.
XX PS (JOHN/) JOHNSON E S.
XX PI Johnson ES;
XX DR WPI; 2002-478534/51.
XX XX
XX PT Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
XX PT long terminal repeats, in a DNA sample from a patient indicates that the
XX PT patient has, or is likely to develop ALSV-induced lung cancer.
XX PS Disclosure; Fig 8; 25pp; English.
XX CC ABL59276-86 represent PCR amplified fragments from a conserved region of
XX CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
XX CC ABL59283 represents a positive control from a chicken tumour induced by
XX CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
XX CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
XX CC which the amplified sequence showed closest homology. The primers used
XX CC for amplification were used to screen for an increased potential for
XX CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
XX CC nucleic acid sequences in DNA from a sample from the patient. The method
XX CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
XX CC 2003 to correct OS field.)
XX SQ Sequence 178 BP; 45 A; 44 C; 44 G; 44 T; 0 U; 1 Other;
XX
Query Match 98.4%; Score 62; DB 6; Length 178;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGTTGTCAC 60
Db 55 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGTTGTCAC 114
Qy 61 CT 62
Db 115 CT 116
XX
RESULT 60
ABLS9278
ID ABL59278 standard; DNA; 181 BP.
XX AC ABL59278;
XX DT 07-AUG-2003 (revised)
XX DT 07-OCT-2002 (first entry)
XX DE Nucleotide sequence of fragment 1832107 from LTR of ALSV.
XX KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
XX OS Avian leukosis virus.

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XX PN US6391555-B1.
XX PD 21-MAY-2002.
XX PF 07-JAN-2000; 2000US-00479770.
XX PR 07-JAN-1999; 99US-0115087P.
XX PS (JOHN/) JOHNSON E S.
XX PI Johnson ES;
XX DR WPI; 2002-478534/51.
XX XX
XX PT Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
XX PT long terminal repeats, in a DNA sample from a patient indicates that the
XX PT patient has, or is likely to develop ALSV-induced lung cancer.
XX PS Disclosure; Fig 8; 25pp; English.
XX CC ABL59276-86 represent PCR amplified fragments from a conserved region of
XX CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
XX CC ABL59283 represents a positive control from a chicken tumour induced by
XX CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
XX CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
XX CC which the amplified sequence showed closest homology. The primers used
XX CC for amplification were used to screen for an increased potential for
XX CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
XX CC nucleic acid sequences in DNA from a sample from the patient. The method
XX CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
XX CC 2003 to correct OS field.)
XX SQ Sequence 181 BP; 45 A; 44 C; 47 G; 44 T; 0 U; 1 Other;
XX
Query Match 98.4%; Score 62; DB 6; Length 181;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGTTGTCAC 60
Db 55 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGTTGTCAC 114
Qy 61 CT 62
Db 115 CT 116
XX
RESULT 61
ABLS9280
ID ABL59280 standard; DNA; 210 BP.
XX AC ABL59280;
XX DT 07-AUG-2003 (revised)
XX DT 07-OCT-2002 (first entry)
XX DE Nucleotide sequence of fragment 1765805B from LTR of ALSV.
XX KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
XX OS Avian leukosis virus.
XX PN US6391555-B1.
XX PD 21-MAY-2002.
XX PF 07-JAN-2000; 2000US-00479770.
XX PR 07-JAN-1999; 99US-0115087P.
XX PS (JOHN/) JOHNSON E S.
XX

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PI Johnson ES;
 XX WPI; 2002-478534/51.
 XX
 PT Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
 PT long terminal repeats, in a DNA sample from a patient indicates that the
 PT patient has, or is likely to develop ALSV-induced lung cancer.
 XX
 PS Disclosure; Fig 8; 25pp; English.
 XX
 CC ABL59276-86 represent PCR amplified fragments from a conserved region of
 CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
 CC ABL59283 represents a positive control from a chicken tumour induced by
 CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
 CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
 CC which the amplified sequence showed closest homology. The primers used
 CC for amplification were used to screen for an increased potential for
 CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
 CC nucleic acid sequences in DNA from a sample from the patient. The method
 CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
 CC 2003 to correct OS field.)
 XX
 SQ Sequence 210 BP; 54 A; 49 C; 53 G; 53 T; 0 U; 1 Other;
 Query Match 98.4%; Score 62; DB 6; Length 210;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGGTGCAC 60
 DB 84 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGGTGCAC 143
 QY 61 CT 62
 DB 144 CT 145
 RESULT 62
 ABL59286
 ID ABL59286 standard; DNA; 211 BP.
 XX
 AC ABL59286;
 XX
 DT 07-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 DE Nucleotide sequence of fragment V01168 from LTR of ALSV.
 KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
 OS Avian leukosis virus.
 XX
 FN US6391555-B1.
 XX
 PD 21-MAY-2002.
 XX
 PF 07-JAN-2000; 2000US-00479770.
 XX
 PR 07-JAN-1999; 99US-0115087P.
 XX
 PA (JOHN/) JOHNSON E S.
 XX
 PI Johnson ES;
 XX
 DR WPI; 2002-478534/51.
 XX
 PT Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
 PT long terminal repeats, in a DNA sample from a patient indicates that the
 PT patient has, or is likely to develop ALSV-induced lung cancer.
 XX
 PS Disclosure; Fig 8; 25pp; English.
 XX
 CC ABL59276-86 represent PCR amplified fragments from a conserved region of

CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
 CC ABL59283 represents a positive control from a chicken tumour induced by
 CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
 CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
 CC which the amplified sequence showed closest homology. The primers used
 CC for amplification were used to screen for an increased potential for
 CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
 CC nucleic acid sequences in DNA from a sample from the patient. The method
 CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
 CC 2003 to correct OS field.)
 XX
 SQ Sequence 211 BP; 56 A; 50 C; 52 G; 53 T; 0 U; 0 Other;
 Query Match 98.4%; Score 62; DB 6; Length 211;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGGTGCAC 60
 DB 83 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGGTGCAC 142
 QY 61 CT 62
 DB 143 CT 144
 RESULT 63
 ABL59276
 ID ABL59276 standard; DNA; 213 BP.
 XX
 AC ABL59276;
 XX
 DT 07-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 DE Nucleotide sequence of fragment R-1366571 from LTR of ALSV.
 KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
 OS Avian leukosis virus.
 XX
 FN US6391555-B1.
 XX
 PD 21-MAY-2002.
 XX
 PF 07-JAN-2000; 2000US-00479770.
 XX
 PR 07-JAN-1999; 99US-0115087P.
 XX
 PA (JOHN/) JOHNSON E S.
 XX
 PI Johnson ES;
 XX
 DR WPI; 2002-478534/51.
 XX
 PT Detecting avian leucosis/sarcoma virus (ALSV) nucleic acids, particularly
 PT long terminal repeats, in a DNA sample from a patient indicates that the
 PT patient has, or is likely to develop ALSV-induced lung cancer.
 XX
 PS Disclosure; Fig 8; 25pp; English.
 XX
 CC ABL59276-86 represent PCR amplified fragments from a conserved region of
 CC the long terminal repeat (LTR) of avian leucosis/sarcoma virus (ALSV).
 CC ABL59283 represents a positive control from a chicken tumour induced by
 CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
 CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
 CC which the amplified sequence showed closest homology. The primers used
 CC for amplification were used to screen for an increased potential for
 CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
 CC nucleic acid sequences in DNA from a sample from the patient. The method
 CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
 CC 2003 to correct OS field.)
 XX

SQ Sequence 213 BP; 56 A; 50 C; 53 G; 53 T; 0 U; 1 Other;
 Query Match 98.4%; Score 62; DB 6; Length 213;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||
 DB 83 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 142
 |||

QY 61 CT 62
 ||
 DB 143 CT 144

RESULT 64
 ID ABL59285
 AC ABL59285;
 XX
 DT 07-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)
 XX
 DE Nucleotide sequence of fragment L29198 from LTR of ALSV.
 XX
 KW Long terminal repeat; LTR; ALSV; lung cancer; ALSV-induced cancer; ss.
 XX
 OS Avian leukosis virus.
 XX
 PN US6391555-B1.
 XX
 PD 21-MAY-2002.
 XX
 PF 07-JAN-2000; 2000US-00479770.
 XX
 PR 07-JAN-1999; 99US-0115087P.
 XX
 PA (JOHN/) JOHNSON E S.
 XX
 PI Johnson ES;
 XX
 DR WPI; 2002-478534/51.
 XX
 PT Detecting avian leukosis/sarcoma virus (ALSV) nucleic acids, particularly
 PT long terminal repeats, in a DNA sample from a patient indicates that the
 PT patient has, or is likely to develop ALSV-induced lung cancer.
 XX
 PS Disclosure; Fig 8; 25pp; English.
 XX
 CC ABL59276-86 represent PCR amplified fragments from a conserved region of
 CC the long terminal repeat (LTR) of avian leukosis/sarcoma virus (ALSV).
 CC ABL59283 represents a positive control from a chicken tumour induced by
 CC ALSV. ABL59284 is also a positive control, and is derived from plasmid
 CC containing ALSV sequences. ABL59285-86 represent subgroup A isolates to
 CC which the amplified sequence showed closest homology. The primers used
 CC for amplification were used to screen for an increased potential for
 CC developing ALSV-induced lung cancer. The method comprises detecting ALSV
 CC nucleic acid sequences in DNA from a sample from the patient. The method
 CC is useful for the detection of ALSV-induced cancer. (Updated on 07-AUG-
 CC 2003 to correct OS field.)
 XX
 SQ Sequence 213 BP; 56 A; 50 C; 53 G; 54 T; 0 U; 0 Other;

Query Match 98.4%; Score 62; DB 6; Length 213;
 Best Local Similarity 100.0%; Pred. No. 4.1e-14;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
 |||
 DB 83 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 142
 |||

QY 61 CT 62

Db 143 CT 144

RESULT 65
 AAT71261
 ID AAT71261 standard; DNA; 565 BP.
 XX
 AC AAT71261;
 XX

XX 30-MAR-1998 (first entry)
 XX
 DE Rous sarcoma virus v-src gene.
 XX

XX Cognate transgene; v-src gene; lymphoma; cellular immunogen; cancer;
 KW self-determinant immunoreactivity; cancer vaccination; breast carcinoma;
 KW colon carcinoma; immunotherapy; proto-oncogene; rous sarcoma virus; ss.
 XX

OS Rous sarcoma virus.

XX W09725860-AL.

XX 24-JUL-1997.

XX 13-JAN-1997; 97WO-US000582.

XX 19-JAN-1996; 96US-0010262P.

XX (UYAL-) UNIV ALLEGHENY HEALTH SCI.

XX Halpern MS, England JM;

XX WPI; 1997-384993/35.

PT Proto-oncogene immunogen - used in vaccine for the prevention and
 PT treatment of cancer.

PS Disclosure; Page 69; 81pp; English.

XX This sequence represents the Rous sarcoma virus v-src cognate transgene
 CC (CRG). Deletion of amino acids 430-433 of the encoded protein renders the
 CC CTG non-transforming. This sequence can be used in the cellular immunogen
 CC of the invention. The cellular immunogen of the invention is for
 CC immunising against the product of a target proto-oncogene, over-
 CC expression of which is associated with cancer, comprises host cells
 CC transfected with a construct containing at least one transgene related to
 CC the proto-oncogene and driven by a strong promoter. The product of the
 CC transgene induces immunoreactivity to host self-determinants on the
 CC product of proto-oncogene. The cellular immunogens are used for
 CC protective vaccination against cancer (e.g. carcinoma of breast or colon,
 CC or various lymphomas) and for immunotherapy of cancer. Use of the
 CC immunogen eliminates the need to isolate immunogenic, HLA host-matched
 CC peptides. The method is not based on immune recognition of a determinant
 CC defined by a cancer-specific mutation and generates a systemic (anti-
 CC metastatic) response

SQ Sequence 565 BP; 148 A; 114 C; 162 G; 141 T; 0 U; 0 Other;

Query Match 98.4%; Score 62; DB 2; Length 565;

Best Local Similarity 100.0%; Pred. No. 5.1e-14;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60

DB 439 TTTAAGTGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 498

QY 61 CT 62

DB 499 CT 500

RESULT 66

AAZ60824

```

ID  AA260824 standard; DNA; 565 BP.
XX
AC  AA260824;
XX
KW  Nucleotide sequence of a cognate transgene of v-src.
DT  16-MAY-2000 (first entry)
DE
DE  Cognate transgene; CTG; tumorigenic; cellular immunogen; immunisation;
XX  proto-oncogene; malignancy; allogenic cell; vaccine; cancer; ss.
XX
OS  Rat sarcoma virus.
XX
XX  WO200004927-A1.
XX
XX  03-FEB-2000.
XX
XX  08-JUL-1999; 99WO-US015594.
XX
XX  24-JUL-1998; 98US-0093965P.
XX
XX  (UVAL-) UNIV ALLEGHNEY HEALTH SCI.
PA  (HALP/) HALPERN M S.
PA  (ENGL/) ENGLAND J M.
XX
XX  Halpern MS, England JM;
XX
XX  WPI; 2000-182543/16.
XX
XX  Cellular immunogens comprising allogenic donor cells transfected with a
PT  construct comprising a proto-oncogene cognate, useful as cancer vaccines.
XX
XX  Disclosure; Page 75-76; 77pp; English.
XX
XX  The present sequence represents a cognate transgene (CTG) which is
CC  rendered non-tumorigenic by deletion of amino acids 9-155. The CTG is
CC  used in the course of the invention. The specification describes a
CC  cellular immunogen for immunizing a host against the effects of the
CC  product of a target proto-oncogene which is associated with a
CC  malignancy. The cellular immunogen comprises allogenic cells transfected
CC  with transgene construct comprising a transgene cognate to target proto-
CC  oncogene and a strong promoter. The cellular immunogen is useful for
CC  vaccinating a host against cancer by inserting the transgene construct
CC  into the body of the host for the expression of the transgene. The method
CC  of the invention is designed to target mutation-driven non-self
CC  determinants. The cellular immunogens induce reactivity for self-
CC  determinants in the over expressed product of tumour associated and over
XX  expressed proto-oncogenes
XX
SQ  Sequence 565 BP; 148 A; 114 C; 162 G; 141 T; 0 U; 0 Other;

Query Match      98.4%; Score 62; DB 3; Length 565;
Best Local Similarity 100.0%; Pred. No. 5.1e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db  439 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 498

Qy  61 CT 62
    ||
Db  499 CT 500

RESULT 67
AAT62602
ID  AAT62602 standard; DNA; 7223 BP.
XX
AC  AAT62602;
XX
XX  25-MAR-2003 (revised)
DT  12-MAY-1997 (first entry)
XX

DE  Luciferase expression vector, pRSVLuc.
XX
KW  NLS; 126-132; SV40 large T antigen; nuclear location signal; transport;
XX  inducible repressor; vector; expression; exogenous; eukaryotic cell;
XX  transgenic animal; model; human disease; ss.
XX
XX  Synthetic.
XX
XX  US5589392-A.
XX
XX  31-DEC-1996.
XX
XX  29-NOV-1993; 93US-00158718.
XX
XX  14-JAN-1991; 91US-00640983.
XX
XX  (STRA-) STRATAGENE.
XX
XX  Short JM;
XX
XX  WPI; 1997-107141/10.
XX
XX  Nucleic acid construct for gene expression - comprising DNA sequences
PT  encoding nuclear transport signal peptide and inducible repressor.
XX
XX  Example 2; Col 43-50; 43pp; English.
XX
XX  DNA constructs encoding a nuclear transport signal operatively linked to
CC  a DNA sequence encoding an inducible repressor are useful as vectors for
CC  expression of exogenous genes in eukaryotic cells in vitro and in vivo,
CC  e.g. for production of transgenic animals as models for human diseases.
CC  The present sequence is that of a luciferase reporter expression vector,
CC  pRSVLuc. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX  Sequence 7223 BP; 1880 A; 1730 C; 1864 G; 1745 T; 0 U; 4 Other;

Query Match      98.4%; Score 62; DB 2; Length 7223;
Best Local Similarity 100.0%; Pred. No. 9.1e-14;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db  2567 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 2626

Qy  61 CT 62
    ||
Db  2627 CT 2628

RESULT 68
AAZ29699
ID  AAZ29699 standard; DNA; 11627 BP.
XX
AC  AAZ29699;
XX
XX  22-MAR-2000 (first entry)
XX
XX  Viral expression vector, RCASBP(A) construct.
XX
XX  Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
KW  viral expression vector; RCASBP(A) construct; replication competent;
KW  Bryan polymerase; BP; 'A' type envelope glycoprotein; mutant Src;
KW  inflammatory disease; arthritis; rheumatoid arthritis; restenosis;
KW  diabetic retinopathy; osteoporosis; cancer; ds.
XX
XX  Synthetic.
XX
XX  Avian sarcoma virus.
XX
XX  Key      Location/Qualifiers
XX  LTR      1..101
XX  repeat_unit 1..21
XX  repeat_tag 1..21
XX  repeat_tag 1..21

```

```

FT misc_feature /rpt_type= DIRECT
FT 22..101
FT /tag= c
FT /note= "5' end unique sequence"
FT CDS 372..2483
FT /tag= d
FT /product= "gag protein"
FT /note= "Proteins of nucleoprotein core of the virion"
FT mat_peptide 372..902
FT /tag= e
FT /label= gag_p19_peptide
FT 388..391
FT /tag= f
FT /note= "Splice donor site"
FT mat_peptide 903..1094
FT /tag= g
FT /label= gag_p10_peptide
FT 1095..1814
FT /tag= h
FT /label= gag_p27_peptide
FT mat_peptide 1843..2108
FT /tag= i
FT /label= gag_p12_peptide
FT 2109..2480
FT /tag= j
FT /label= gag_pi5_peptide
FT CDS 2501..5189
FT /tag= k
FT /product= "Reverse transcriptase polymerase (pol)"
FT mat_peptide 2501..4216
FT /tag= l
FT /label= Polymerase_pol_RT
FT mat_peptide 4217..5186
FT /tag= m
FT /label= Polymerase_pol_IN
FT 5075..5078
FT /tag= n
FT /note= "env splice acceptor site"
FT CDS 5245..6882
FT /tag= o
FT /product= "Envelope protein (env)"
FT mat_peptide 5245..6264
FT /tag= p
FT /label= env_gp85_peptide
FT mat_peptide 6265..6879
FT /tag= q
FT /label= env_gp37_peptide
FT misc_recomb 6983..6986
FT /tag= r
FT /note= "Clai splice acceptor site"
FT misc_feature 7154..7165
FT /tag= s
FT /label= ppt
FT LTR 7166..7494
FT /tag= t
FT misc_feature 7166..7394
FT /tag= u
FT /note= "3' end unique sequence"
FT repeat_unit 7395..7415
FT /tag= v
FT /rpt_type= DIRECT
FT 7416..7494
FT /tag= w
FT /note= "5' end unique sequence"
FT misc_feature 7649..11258
FT /tag= x
FT /label= pB322_vector
FT 11394..11623
FT /tag= y
FT /note= "3' end unique sequence"
FT WO961590-A1.
XX
XX

```

```

PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US011780.
XX
XX 29-MAY-1998; 98US-0087220P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Cheresch DA, Eliceiri B, Schwartzberg PL;
XX
XX WPI; 2000-116335/10.
XX
XX Using tyrosine kinase Src for modulating angiogenesis in tissues useful
XX in, e.g. treatment of chronic articular rheumatism.
XX
XX Claim 15; Page 59-66; 80pp; English.
XX
XX The present DNA sequence is the viral expression vector, RCASBP(A)
XX construct. This vector is based on a replication competent avian sarcoma
XX virus with an enhanced Bryan polymerase (Bp) and is specific for the 'A'
XX type envelope glycoprotein expressed on normal avian cells. The vector
XX expresses Src protein or modified Src, that can be used to modulate
XX angiogenesis. When the Src protein is inactivated, angiogenesis is
XX inhibited, while when it is activated, angiogenesis is potentiated. This
XX modified or mutant Src can be used to treat inflammatory diseases like,
XX arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis,
XX osteoporosis and cancer associated disorders
XX
XX Sequence 11627 BP; 2796 A; 2808 C; 3324 G; 2699 T; 0 U; 0 Other;
XX
XX Query Match 98.4%; Score 62; DB 3; Length 11627;
XX Best Local Similarity 100.0%; Pred. No. 1e-13;
XX Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTTAAGTGCCTAGCTCGATACATATAACGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 7367 TTTAAGTGCCTAGCTCGATACATATAACGCCATTGACCATTCACCATTTGGTGTGCAC 7426
QY 61 CT 62
Db 7427 CT 7428

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RESULT 69
ABZ23249
ID ABZ23249 standard; DNA; 2245 BP.
XX
AC ABZ23249;
XX
XX 24-MAR-2003 (first entry)
XX
XX Lac repressor operated p21-expression cassette and RSV-LTR promoter.
XX
XX Lac repressor; p21; RSV; LTR promoter; cell cycle inhibitor protein;
XX protein production; anchorage-independent producer cell line; es.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX promoter 1..563
XX /tag= a
XX /note= "RSV-LTR promoter"
XX intron 564..1051
XX /tag= b
XX /note= "SV40 small t antigen intron"
XX misc_feature 1052..1907
XX /tag= c
XX /note= "p21 coding sequence"
XX polyA_signal 1908..2245
XX /tag= d
XX /note= "thymidine kinase polyA site"
XX
XX WO200299100-A2.
XX

```

XX 12-DEC-2002.
 XX 03-JUN-2002; 2002WO-BP006054.
 XX 01-JUN-2001; 2001GB-00013318.
 XX (LONZ) LONZA BIOLOGICS PLC.
 XX Al-Rubeai M, Shuttlesworth J;
 XX WPI; 2003-148669/14.
 XX Producing recombinant protein, particularly for maximizing or enhancing
 PT e.g. therapeutic protein production, by co-expressing protein with
 PT recombinant cell cycle inhibitor protein (p21) in producer cell line.
 XX Example 1; Page 15-16; 33pp; English.
 XX The present sequence represents a lac repressor operated p21-expression
 CC cassette comprising the Rous sarcoma virus (RSV)-LTR promoter. p21 is a
 CC cell cycle inhibitor protein. The present sequence is used to produce
 CC vectors for use in the method of the invention. The specification
 CC describes a method for producing a protein, preferably a recombinant
 CC protein, in a mammalian anchorage-independent producer cell line. The
 CC method comprises co-expressing with the protein in the producer cell line
 CC a recombinant cell cycle inhibitor protein (preferably p21). The method
 CC is useful for producing a recombinant protein in a producer cell line.
 CC This is particularly useful for maximizing or enhancing the production of
 CC e.g. therapeutic proteins at an industrial scale
 XX Sequence 2245 BP; 532 A; 555 C; 625 G; 533 T; 0 U; 0 Other;
 SQ Query Match 96.8%; Score 61; DB 7; Length 2245;
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 DB 506 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 565
 QY 61 C 61
 DB 566 C 566
 RESULT 70
 AAS15665
 ID AAS15665 standard; DNA; 262 BP.
 XX AAS15665;
 AC AAS15665;
 XX 29-JAN-2002 (first entry)
 XX Human respiratory syncytial virus promoter.
 XX Ecdysone receptor; EcR; ligand binding domain; ds; retinoid X receptor;
 KW RXalpha; DNA-binding domain; RSV promoter; transactivation domain;
 KW nuclear receptor; ultraspiracle; gene therapy; protein production;
 KW antibody production; high throughput screening; HTS; transgenic plant;
 KW transgenic animal.
 XX Human respiratory syncytial virus.
 OS Human respiratory syncytial virus.
 XX WO200170816-A2.
 XX 27-SEP-2001.
 XX 21-MAR-2001; 2001WO-US009050.
 XX 22-MAR-2000; 2000US-0191355P.
 XX 20-FEB-2001; 2001US-0269799P.
 XX

PA (ROHM) ROHM & HAAS CO.
 XX Palli SR, Kapitkaya MZ, Cress DE;
 XX WPI; 2001-656841/75.
 XX Ecdysone and retinoid X receptor based inducible gene expression systems
 PT for use in e.g. gene therapy, large scale production of proteins and cell
 PT based high-throughput screening assays.
 XX Example 1; Page 141; 144pp; English.
 XX The invention relates to Ecdysone and retinoid X receptor based inducible
 CC gene expression systems useful for modulating gene expression in host
 CC cells. The gene expression system encodes a polypeptide with a DNA-
 CC binding domain recognizes a response element associated with a gene whose
 CC expression is to be modulated and/or a ligand binding domain (LBD)
 CC comprising a LBD from a nuclear receptor and a second gene expression
 CC cassette capable of being expressed in a host cell comprising a
 CC polynucleotide sequence encoding a second polypeptide comprising a trans-
 CC activation domain and/or a LBD comprising a LBD from a nuclear receptor
 CC other than ultraspiracle (USP) (the trans-activation domain is from a
 CC nuclear receptor other than an ecdysone receptor, a retinoid X receptor
 CC or a USP receptor and the LBDs from the first and second polypeptides are
 CC different and dimerize). The ecdysone and retinoid X receptor based
 CC inducible gene expression systems useful for modulating gene expression
 CC in host cells, for use in gene therapy, large scale production of
 CC proteins and antibodies, cell-based high-throughput screening assays
 CC (HTS), functional genomic and regulation of traits in transgenic plants
 CC and animals. The present sequence represents promoter from human
 CC respiratory syncytial virus (RSV) which is used in an inducible gene
 CC expression system of the invention
 XX Sequence 262 BP; 79 A; 53 C; 64 G; 66 T; 0 U; 0 Other;
 SQ Query Match 95.9%; Score 60.4; DB 4; Length 262;
 Best Local Similarity 98.4%; Pred. No. 1.8e-13;
 Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 DB 201 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 260
 QY 61 CT 62
 DB 261 CT 262
 RESULT 71
 ABL90071
 ID ABL90071 standard; cDNA; 766 BP.
 XX ABL90071;
 AC ABL90071;
 XX 24-MAY-2002 (first entry)
 XX Human polynucleotide SEQ ID NO 633.
 DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 XX anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;
 KW nuclear receptor; ultraspiracle; gene therapy; protein production;
 KW antibody production; high throughput screening; HTS; transgenic plant;
 KW transgenic animal.
 XX Human respiratory syncytial virus.
 OS Human respiratory syncytial virus.
 XX WO200170816-A2.
 XX 27-SEP-2001.
 XX 21-MAR-2001; 2001WO-US009050.
 XX 22-MAR-2000; 2000US-0191355P.
 XX 20-FEB-2001; 2001US-0269799P.
 XX

XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Birse CE, Rosen CA;
XX DR WPI; 2002-122018/16.
XX PT P-PSDB; ABB99662.
XX
XX PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
XX PT prevention of neural, immune system, muscular, reproductive,
XX PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
XX PT disorders.
XX
XX PS Claim 4; SEQ ID NO 633; 2081pp + Sequence Listing, English.
XX
XX CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
XX CC (ABB99040-ABB90444) useful for preventing, treating or ameliorating
XX CC medical conditions e.g. by protein or gene therapy. The genes are
XX CC isolated from a range of human tissues disclosed in the specification.
XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
XX CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
XX CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX CC infectious diseases such as viral, bacterial, fungal and parasitic
XX CC infections. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 766 BP; 172 A; 206 C; 191 G; 191 T; 0 U; 6 Other;

Query Match 95.9%; Score 60.4; DB 6; Length 766;
Best Local Similarity 98.4%; Pred. No. 2.3e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTAAAGTGCCTAGCTCGATACAAATAAACGCCATTGACCATTCACACATTGGTGTGCAC 60
Db 169 TTTAAGTGCCTAGCTCGATACAAATAAACGCCATTGACCATTCACACATTGGTGTGCAC 228
|||
QY 61 CT 62
|||
Db 229 CT 230

RESULT 72
AAC92489
ID AAC92489 standard; DNA; 858 BP.
XX AAC92489;
XX
XX DT 26-MAR-2001 (first entry)
XX
XX DE Fragment of RSV DNA including tandem repeat LTR and non-coding region.
XX
XX KW Integrase; transgenic animal; transgenic bird; gene therapy; cancer; ds.
XX
XX OS Rous sarcoma virus.
XX
XX PN WO200075342-A1.
XX
XX PD 14-DEC-2000.
XX
XX PF 27-APR-2000; 2000WO-JP002785.
XX
XX PR 04-JUN-1999; 99JP-00158351.
XX
XX PA (NIPPON) NIPPON INST BIOLOGICAL SCIENCE.
XX
XX PI Katsumata A, Hoshi S, Ihara T, Ueda S;

XX WPI; 2001-061729/07.
XX
XX PT Plasmid vector for efficient insertion of foreign DNA into host cells to
XX PT give transforms with stable quality, useful e.g. in producing DNA
XX PT vaccines on large scale, and in gene therapy with ease and safely and
XX PT without pathogenicity.
XX
XX PS Disclosure; Page 88-89; 94pp; Japanese.
XX
XX CC This invention relates to a vector which consists of an integrase gene, a
XX CC regulatory region of DNA involved in the expression of the integrase
XX CC gene, and a DNA fragment constituting a recognition region used in the
XX CC catalysis of the integrase in the integrase reaction. The invention
XX CC includes methods for the production of transgenic animals and birds using
XX CC the vector of the invention. The plasmid vector can be for inserting
XX CC foreign DNA into host cells to yield transformants. The transformants may
XX CC be useful in producing DNA vaccines, and in gene therapy against cancer,
XX CC congenital genetic diseases or infections. The present sequence
XX CC represents a fragment of DNA from Rous sarcoma virus, including tandem
XX CC repeat LTRs and adjacent non-coding region. The DNA fragment is used in
XX CC the production of the vector of the invention
XX
XX SQ Sequence 858 BP; 215 A; 202 C; 246 G; 195 T; 0 U; 0 Other;

Query Match 95.9%; Score 60.4; DB 5; Length 858;
Best Local Similarity 98.4%; Pred. No. 2.3e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTAAAGTGCCTAGCTCGATACAAATAAACGCCATTGACCATTCACACATTGGTGTGCAC 60
Db 86 TTTAAGTGCCTAGCTCGATACAAATAAACGCCATTGACCATTCACACATTGGTGTGCAC 145
|||
QY 61 CT 62
|||
Db 146 CT 147

RESULT 73
ABK10062
ID ABK10062 standard; DNA; 5283 BP.
XX
XX AC ABK10062;
XX
XX DT 21-MAY-2002 (first entry)
XX
XX DE Expression vector construct pVGI.1 containing VEGF-2 insert.
XX
XX KW Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1;
XX KW chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a;
XX KW allergic reaction; organ rejection; inflammatory condition; arrhythmia;
XX KW hyperproliferative disorder; viral infection; bacterial infection;
XX KW fungal infection; parasitic infection; cardiovascular disorder; embolism;
XX KW heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.
XX
XX OS Synthetic.
XX
XX PN WO200211769-A1.
XX
XX PD 14-FEB-2002.
XX
XX PF 03-AUG-2001; 2001WO-US024658.
XX
XX PR 04-AUG-2000; 2000US-0223276P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Coleman TA;
XX
XX DR WPI; 2002-217153/27.
XX
XX PT Isolated nucleic acid having expression vector construct with vascular
XX PT endothelial growth factor-2 insert, useful for treating chronic limb

PT	New fusion proteins having an extracellular domain with biotin-binding activity, used to target biotinylated molecules to specific sites in tissues.
XX	
XX	Disclosure; Page 15-21; 23pp; English.
XX	
CC	This invention describes a novel protein (A) which comprises a membrane-spanning domain and an extracellular domain (ECD), where the ECD comprises biotin-binding activity. Using the proteins or encoding nucleic acid molecules it is possible to target biotinylated molecules to specific sites in tissues. Molecules targeted in this way may be taken up by the tissues or cells by endocytosis, allowing the molecules to exert their effects within or on the cell. This sequence encodes a bovine scavenger receptor class A/avidin fusion protein which is used in the description of the invention
CC	
XX	Sequence 5177 BP; 1356 A; 1222 C; 1390 G; 1209 T; 0 U; 0 Other;
XX	
XX	Query Match 94.9%; Score 59.8; DB 2; Length 5177;
XX	Best Local Similarity 96.8%; Pred. No. 6e-13;
XX	Matches 61; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 TTTAAGTGCTAGTCGATGACATTAAGCCGCAATTGACATTTCACCACTTGGTGTGCAC 60
DB	3307 TTTAAGTGCTAGTCGATGACATTAAGCCGCAATTGACATTTCACCACTTGGTGTGCAC 3366
QY	61 CTC 53
DB	3367 CTC 3369
XX	
XX	RESULT 75
XX	AAQ75973
ID	AAQ75973 standard; cDNA; 4965 BP.
AC	AAQ75973;
XX	
DT	25-MAR-2003 (revised)
XX	
DT	23-AUG-1995 (first entry)
XX	
DE	pHLA-B7/beta-2 microglobulin expression vector.
XX	
XX	expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7; light beta-2 microglobulin; class I major histocompatibility complex; MHC; bicistronic mRNA; human leukocyte antigen; HLA;
KW	covalently closed circular DNA; ds.
KW	
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
LTR	1..529
FT	/*tag= a
FT	/note= "Rous sarcoma virus LTR promoter domain, derived for the Schmidt-Rupin strain nucleotides 8673-9146. This region also includes a 56 bp region of a synthetic oligonucleotide which modifies this regulatory sequence to effect a higher level of expression of downstream sequences. The oligonucleotide removes a polyadenylation signal sequence originally found in the RSV DNA sequence."
FT	misc_signal 531..534
FT	/*tag= b
FT	/label= consensus_Kozak_signal_sequence
FT	535..1620
CDS	/*tag= c
FT	/note= "HLA-B7 heavy chain open reading frame"
FT	535..606
FT	/*tag= d
FT	/note= "encodes putative signal peptide of the HLA-B7 heavy chain"
FT	607..1620
FT	/*tag= e
FT	/note= "encodes putative HLA-B7 heavy chain mature peptide"
FT	

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FT 3'UTR peptide"
FT 1621..1853
FT /*tag= f
FT /note= "3' untranslated sequence of HLA-B7 heavy chain
FT mRNA"
FT 1854..1888
FT /*tag= g
FT /note= "multiple cloning site, forms a junction between
FT the HLA-B7 sequence and the EMCV-CITE sequence, and is
FT used to facilitate subcloning"
FT 1889..2479
FT /*tag= h
FT /note= "murine encephalomyocarditis CAP-independent
FT translational enhancer (EMCV-CITE); taken from
FT nucleotides 255-843 of cloned EMCV genomic DNA. It is a
FT non-coding regulatory sequence functioning as an internal
FT entry point for the eukaryotic ribosomal subunits when
FT located within a mRNA mol. . It enables the translational
FT start codon of the beta-2 microglobulin, downstream of
FT the HLA-B7 stop codon on this bicistronic mRNA to be
FT recognised by the ribosome"
FT 2480..2839
FT /*tag= i
FT /note= "encodes beta-2 microglobulin; this cDNA is deriv.
FT from chimpanzee (differs to the human cDNA by only 4
FT bases)"
FT 2840..2846
FT /*tag= j
FT /note= "3' untranslated region of the beta-2
FT microglobulin mRNA"
FT 2847..2870
FT /*tag= k
FT /note= "synthetic linker"
FT 2979..2984
FT /*tag= l
FT 3112..3151
FT /*tag= m
FT /note= "synthetic linker to facilitate cloning"
FT complement(3151..3967)
FT /*tag= n
FT /note= "kanamycin resistance gene open reading frame; the
FT gene is taken from the transposable element Tn903"
FT 4014..4965
FT /*tag= o
FT /note= "pBR322 backbone contg. bacterial origin of
FT replication, it represents nucleotides 2244-3193"
FT
FT
FT WO9429469-A2.
FT
FT 22-DEC-1994.
FT
FT 27-MAY-1994; 94WO-US006069.
FT
FT 07-JUN-1993; 93US-00074344.
FT
FT (VICA-) VICAL INC.
FT (UNMI ) UNIV MICHIGAN.
FT
FT Nabel GJ, Nabel EG, Lew D, Marquet M;
FT WPI, 1995-036494/05.
FT
FT New vectors for gene therapy, partic for tumours - comprising genetic
FT material encoding one or more cistron(s) which express immunogenic or
FT therapeutic peptide(s).
FT
FT Claim 8; Page 41-42; 50pp; English.
FT
FT The pHIA-B7/beta-2 microglobulin plasmid expression vector, in addition
FT to the kanamycin resistance gene, contains the plasmid DNA encoding the
FT heavy (human HLA-B7) and light (beta-2 microglobulin) proteins of a class
FT I major histocompatibility complex (MHC) antigen. The plasmid is
FT designed to express these two proteins via a bicistronic mRNA in

```

```

CC eukaryotic cells. Initiation of transcription of the mRNA is dependent on
CC a Rous Sarcoma Virus (RSV) promoter sequence deriv. from the 3' long
CC terminal repeat. Termination of transcription is dependent upon the
CC polyadenylation signal sequence deriv. from the bovine growth hormone
CC gene. Eukaryotic cell translation of the heavy chain is regulated by the
CC 5' cap-dependent protein start site. Translation of the light chain is
CC controlled by the CITE. Finally the replication of the plasmid in
CC bacterial cells is controlled by the presence of a bacterial origin of
CC replication. The vector is used partic. for the treatment of neoplastic
CC disease, eg. melanoma, and provides enhanced gene delivery and expression
CC in vivo. (Updated on 25-MAR-2003 to correct PN field.)
XX

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SQ Sequence 4965 BP; 1171 A; 1293 C; 1338 G; 1163 T; 0 U; 0 Other;

Query Match 92.4%; Score 58.2; DB 2; Length 4965;
 Best Local Similarity 95.2%; Pred. No. 2.5e-12;
 Matches 60; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 461 TTTAAGTGGCTAGCTCGATACATCTCTAGACGCCATTGGACCATTCACACATTGGTGTGCAC 520

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QY 61 CTC 63

Db 521 CTC 523

Search completed: March 11, 2004, 08:23:05
 Job time : 56.7357 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 08:11:32 ; Search time 11.6365 Seconds
(without alignments)
3004.511 Million cell updates/sec

Title: US-09-733-368A-1 COPY 550 612

Perfect score:

Sequence: 1 t t t a a g t g c c t a g c t g a t a a c c a c a t t g g t g t g c a c c t c 63

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Database : Issued Patents NA:*
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3: /cgm2_6/ptdata/2/ina/6A_COMB.seq.*
4: /cgm2_6/ptdata/2/ina/6B_COMB.seq.*
5: /cgm2_6/ptdata/2/ina/PTCTUS_COMB.seq.*
6: /cgm2_6/ptdata/2/ina/backfies1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
C 1	63	100.0	4059	2	US-08-564-313-2	Sequence 2, Appli
C 2	63	100.0	4059	5	PCT-US94-03069-2	Sequence 2, Appli
C 3	63	100.0	5653	1	US-08-073-836-3	Sequence 3, Appli
C 4	63	100.0	5653	1	US-08-235-277-1	Sequence 1, Appli
C 5	63	100.0	6836	4	US-09-479-122-18	Sequence 18, Appli
C 6	63	100.0	6836	4	US-09-484-997-18	Sequence 18, Appli
C 7	63	100.0	6836	4	US-09-481-355-18	Sequence 18, Appli
C 8	63	100.0	6836	4	US-09-481-282-18	Sequence 18, Appli
C 9	63	100.0	6836	4	US-09-455-659A-18	Sequence 18, Appli
C 10	63	100.0	6836	4	US-09-484-996-18	Sequence 18, Appli
C 11	63	100.0	6836	4	US-09-479-123-18	Sequence 18, Appli
C 12	63	100.0	6926	1	US-08-470-299-2	Sequence 2, Appli
C 13	63	100.0	7492	4	US-09-295-141-5	Sequence 5, Appli
C 14	63	100.0	8591	1	US-08-462-659A-6	Sequence 6, Appli
C 15	63	100.0	8591	1	US-08-462-659A-8	Sequence 8, Appli
C 16	63	100.0	8591	1	US-08-123-659A-6	Sequence 6, Appli
C 17	63	100.0	8591	1	US-08-123-659A-8	Sequence 8, Appli
C 18	63	100.0	8591	1	US-08-464-247A-6	Sequence 6, Appli
C 19	63	100.0	8591	1	US-08-464-247A-8	Sequence 8, Appli
C 20	63	100.0	8591	1	US-08-464-248A-6	Sequence 6, Appli
C 21	63	100.0	8591	1	US-08-464-248A-8	Sequence 8, Appli
C 22	63	100.0	9737	4	US-09-479-122-22	Sequence 22, Appli
C 23	63	100.0	9737	4	US-09-479-122-22	Sequence 22, Appli
C 24	63	100.0	9737	4	US-09-479-122-28	Sequence 28, Appli
C 25	63	100.0	9737	4	US-09-484-997-22	Sequence 22, Appli
C 26	63	100.0	9737	4	US-09-484-997-23	Sequence 23, Appli
C 27	63	100.0	9737	4	US-09-484-997-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1

US-08-564-313-2/c
; Sequence 2, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:

; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,313
; FILING DATE: 01-DEC-1995

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Israelser, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033CP1

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7

; US-08-564-313-2
Query Match 100.0%; Score 63; DB 2; Length 4059;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2954 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 2895

QY 61 CTC 63
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Db 2894 CTC 2892

RESULT 2

PCT-US94-06069-2/c
; Sequence 2, Application PC/TUS9406069

GENERAL INFORMATION:

; APPLICANT: Vical Incorporated
; APPLICANT: Regents of the University of Michigan
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary

; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06069
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Israelser, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033VPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN: HLA-B7

; PCT-US94-06069-2
Query Match 100.0%; Score 63; DB 5; Length 4059;
Best Local Similarity 100.0%; Pred. No. 4.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 60
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Db 2954 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACACATTGGTGTGCAC 2895

QY 61 CTC 63
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Db 2894 CTC 2892

RESULT 3

US-08-073-836-3
; Sequence 3, Application US/08073836
; Patent No. 5650306
; GENERAL INFORMATION:

; APPLICANT: Nabel, Gary J.
; APPLICANT: Yang, Zhi-yong
; APPLICANT: Liu, Jinsong
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACIDS FOR INHIBITING
; TITLE OF INVENTION: HIV GENE EXPRESSION

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States of America
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,836
FILING DATE: 07-JUN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UM 9646
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-073-836-3

Query Match 100.0%; Score 63; DB 1; Length 5653;
Best Local Similarity 100.0%; Pred. No. 5.3e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
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DB 542 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 601
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QY 61 CTC 63
DB 602 CTC 604

RESULT 4
US-08-235-277-1
Sequence 1, Application US/08235277
Patent No. 5733543
GENERAL INFORMATION:
APPLICANT: NABEL, GARY J
APPLICANT: WOFFENDIN, CLIVE
APPLICANT: YANG, NIN-SUN
APPLICANT: SHERBY, MICHAEL J
TITLE OF INVENTION: INTRODUCTION OF HIV-PROTECTIVE GENES
TITLE OF INVENTION: INTO CELLS BY PARTICLE-MEDIATED GENE TRANSFER
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,277
FILING DATE: 29-APR-1994

CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5733543man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 6042-008-68
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248955 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Other nucleic acid
US-08-235-277-1

Query Match 100.0%; Score 63; DB 1; Length 5653;
Best Local Similarity 100.0%; Pred. No. 5.3e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
|||||
DB 542 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 601
|||||

QY 61 CTC 63
DB 602 CTC 604

RESULT 5
US-09-479-122-18
Sequence 18, Application US/09479122
Patent No. 6410266
GENERAL INFORMATION:
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHERR, BRUCE
APPLICANT: RUNDLETT, STEPHEN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: ENDOGENOUS GENES
FILE REFERENCE: 0221-0003C
CURRENT APPLICATION NUMBER: US/09/479,122
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 09/276,820
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 09/159,643
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 08/941,223
PRIOR FILING DATE: 1997-09-26
PRIOR APPLICATION NUMBER: 09/263,814
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/253,022
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 18
LENGTH: 6836
TYPE: DNA
ORGANISM: Homo sapiens
US-09-479-122-18

Query Match 100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
|||||
DB 1760 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 1819
|||||

QY 61 CTC 63
DB 1820 CTC 1822

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-481-355-18

Query Match      100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAAGCCATTTGACCAATTCACACATTGGTGTGCAC 60
Db      1760 TTTAAGTGCCTAGCTCGATACATAAAGCCATTTGACCAATTCACACATTGGTGTGCAC 1819
QY      61 CTC 63
Db      1820 CTC 1822

RESULT 8
US-09-481-282-18
; Sequence 18, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-481-282-18

Query Match      100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAAGCCATTTGACCAATTCACACATTGGTGTGCAC 60
Db      1760 TTTAAGTGCCTAGCTCGATACATAAAGCCATTTGACCAATTCACACATTGGTGTGCAC 1819
QY      61 CTC 63
Db      1820 CTC 1822

RESULT 9
US-09-455-659A-18
; Sequence 18, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820

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; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-455-659A-18

Query Match      100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 60
    |||||
Db 1760 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 1819

QY 61 CTC 63
    |||
Db 1820 CTC 1822

RESULT 10
US-09-484-996-18
; Sequence 18, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-996-18

Query Match      100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 60
    |||||
Db 1760 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 1819

QY 61 CTC 63
    |||
Db 1820 CTC 1822
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RESULT 11
US-09-479-123-18
; Sequence 18, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-479-123-18

Query Match      100.0%; Score 63; DB 4; Length 6836;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 60
    |||||
Db 1760 TTTAAGTGGCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATTTGGTGTGCAC 1819

QY 61 CTC 63
    |||
Db 1820 CTC 1822

RESULT 12
US-08-470-299-2
; Sequence 2, Application US/08470299
; Patent No. 5783181
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael J.
; APPLICANT: Murphy, Kay E.
; APPLICANT: Chapman, Conrad G.
; APPLICANT: Clinkenbeard, Helen E.
; APPLICANT: Young, Peter R.
; APPLICANT: Shatzman, Allan R.
; TITLE OF INVENTION: No. 5783181el Compounds
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,299
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P31005C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5024
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; US-08-470-299-2

Query Match
Best Local Similarity 100.0%; Score 63; DB 1; Length 6926;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 709 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 768

QY 61 CTC 63
    |||
Db 769 CTC 771

RESULT 13
US-09-299-141-5
; Sequence 5, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SITHONG
; APPLICANT: BYRNE, BARRY J.
; APPLICANT: MORGAN, MICHAEL
; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
; FILE REFERENCE: 4300.011800
; CURRENT APPLICATION NUMBER: US/09/299,141
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: 60/083,025
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ IDS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7492
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
; US-09-299-141-5

Query Match
Best Local Similarity 100.0%; Score 63; DB 4; Length 7492;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCCATTGACCATTCACCATTTGGTGTGCAC 86

QY 61 CTC 63
    |||
Db 87 CTC 89

RESULT 14
US-08-462-859A-6
; Sequence 6, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: Amyloid Precursor and Method of
; USING SAME TO ACCESS AGENTS WHICH DOWN-REGULATE FORMATION
; OF B-AMYLOID PEPTIDE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; APPLICATION NUMBER: US/08/462,859A
;; FILING DATE: 05-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barnhard, Elizabeth M.
;; REGISTRATION NUMBER: 31,088
;; REFERENCE/DOCKET NUMBER: 31,844-04
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (201)831-3246
;; TELEFAX: (201)831-3305
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8591 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 2393..3853
US-08-462-859A-B

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCAATTGGTGTGCAC 60
Db 5177 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCAATTGGTGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 16
US-08-123-659A-6
; Sequence 6, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3853
US-08-123-659A-8

;; LENGTH: 8591 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: circular
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 2393..3868
US-08-123-659A-6

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCAATTGGTGTGCAC 60
Db 5177 TTTAAGTGCTAGCTCGATACATAAAGCCATTGTGACCATTCACCAATTGGTGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 17
US-08-123-659A-8
; Sequence 8, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (518)475-0611
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3853
US-08-123-659A-8

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 5177 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 5236
QY 61 CTC 63
Db 5237 CTC 5239

RESULT 18
US-08-464-247A-6
; Sequence 6, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3868
; US-08-464-247A-6

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 5177 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 5236
QY 61 CTC 63
Db 5237 CTC 5239

RESULT 19
US-08-464-247A-8
; Sequence 8, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
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```
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,247A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2393..3853
; US-08-464-247A-8

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 5177 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 5236
QY 61 CTC 63
Db 5237 CTC 5239

RESULT 20
US-08-464-248A-6
; Sequence 6, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3305
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8591 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2393..3868
US-08-464-248A-6

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGGACCAATTCACCAATTCGTTGGTGCAC 60
Db 5177 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGGACCAATTCACCAATTCGTTGGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 21
US-08-464-248A-8
Sequence 8, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Virek, M. P.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246

TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8591 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2393..3853
US-08-464-248A-8

Query Match 100.0%; Score 63; DB 1; Length 8591;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGGACCAATTCACCAATTCGTTGGTGCAC 60
Db 5177 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGGACCAATTCACCAATTCGTTGGTGCAC 5236

QY 61 CTC 63
Db 5237 CTC 5239

RESULT 22
US-09-479-122-22
Sequence 22, Application US/09479122
Patent No. 6410266
GENERAL INFORMATION:
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHERF, BRUCE
APPLICANT: RUNDLETT, STEPHEN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: ENDOGENOUS GENES
FILE REFERENCE: 0221-0003C
CURRENT APPLICATION NUMBER: US/09/479,122
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 09/276,820
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 09/159,643
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 08/941,223
PRIOR FILING DATE: 1997-09-26
PRIOR APPLICATION NUMBER: 09/263,814
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 09/253,022
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 9737
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (8347)
OTHER INFORMATION: a, c, t, g, other or unknown
NAME/KEY: modified_base
LOCATION: (8499)
OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-22

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGGACCAATTCACCAATTCGTTGGTGCAC 60
Db 1613 TTTAAGTGGCTAGCTCGATACAAATAAAGCCATTGGACCAATTCACCAATTCGTTGGTGCAC 1672

QY 61 CTC 63


```
Db      1673 CTC 1675

RESULT 23
US-09-479-122-23
; Sequence 23, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; TYPE: DNA
; LENGTH: 9737
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-23

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
      |||||
Db      1613 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1672

QY      61 CTC 63
      |||
Db      1673 CTC 1675

RESULT 25
US-09-484-997-22
; Sequence 22, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; TYPE: DNA
; LENGTH: 9737
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-22

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
      |||||
Db      1613 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1672

QY      61 CTC 63
      |||
Db      1673 CTC 1675

RESULT 24
US-09-479-122-28
; Sequence 28, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003C
; CURRENT APPLICATION NUMBER: US/09/479,122
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
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; NAME/KEY: MODIFIED_base
; LOCATION: (8347)
; OTHER INFORMATION: 3 3 4 2 other[illegible]

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; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-22

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 CTC 63
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Db      1673 CTC 1675

RESULT 29
US-09-481-355-23
; Sequence 23, Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-23

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1613 TTTAAGTCCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATGTTGTGAC 1672

QY      61 CTC 63
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Db      1673 CTC 1675

RESULT 30
US-09-481-355-28
; Sequence 28, Application US/09481355
; Patent No. 6524824
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; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; CURRENT FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-28

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATGTTGTGAC 60
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Db      1613 TTTAAGTCCTAGCTCGATACATAAAGCCCAATTGACCAATTCACCAATGTTGTGAC 1672

QY      61 CTC 63
        |||
Db      1673 CTC 1675

RESULT 31
US-09-481-382-22
; Sequence 22, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-22

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1613 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGGACCATTCACCATTTGGTGTGCAC 1672

Qy 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 32
US-09-481-282-23
; Sequence 23, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-23

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1613 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGGACCATTCACCATTTGGTGTGCAC 1672

Qy 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 33
US-09-481-282-28
; Sequence 28, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
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; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-28

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1613 TTTAAGTGCTAGCTCGATCAATAAAGCCATTGGACCATTCACCATTTGGTGTGCAC 1672

Qy 61 CTC 63
|||
Db 1673 CTC 1675

RESULT 34
US-09-455-659A-22
; Sequence 22, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
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Db 1673 CTC 1675
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: modified_base
LOCATION: (8347)
OTHER INFORMATION: a, c, t, g, other or unknown
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NAME/KEY: modified_base
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OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

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Best Local Similarity 100.0%; Pred. No. 6.1e-15;
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QY 61 CTC 63
Db 1673 CTC 1675
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ORGANISM: Homo sapiens
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NAME/KEY: modified_base
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OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

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Best Local Similarity 100.0%; Pred. No. 6.1e-15;
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QY 61 CTC 63
Db 1673 CTC 1675
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OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 1672
QY 61 CTC 63
Db 1673 CTC 1675
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: modified_base
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OTHER INFORMATION: a, c, t, g, other or unknown
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NAME/KEY: modified_base
LOCATION: (8499)
OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
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QY 61 CTC 63
Db 1673 CTC 1675
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ORGANISM: Homo sapiens
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NAME/KEY: modified_base
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OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
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QY 61 CTC 63
Db 1673 CTC 1675
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (8347)
OTHER INFORMATION: a, c, t, g, other or unknown
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NAME/KEY: modified_base
LOCATION: (8499)
OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

Query Match 100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
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QY 61 CTC 63
Db 1673 CTC 1675
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: modified_base
LOCATION: (8347)
OTHER INFORMATION: a, c, t, g, other or unknown
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NAME/KEY: modified_base
LOCATION: (8499)
OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-22

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; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-484-996-22

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Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTC 63
Db 1673 CTC 1675

RESULT 38
US-09-484-996-23
; Sequence 23, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-484-996-23
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; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-484-996-23

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CTC 63
Db 1673 CTC 1675

RESULT 39
US-09-484-996-28
; Sequence 28, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
; US-09-484-996-28

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1613 TTTAAGTGCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGTGCAC 1672

QY 61 CTC 63
Db 1673 CTC 1675

RESULT 40
US-09-479-123-22
; Sequence 22, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
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; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
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; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-22

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1613 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCATTTGGTGGTGCAC 1672

QY      61 CTC 63
Db      1673 CTC 1675

RESULT 41
US-09-479-123-23
; Sequence 23, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-28

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTAAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCATTTGGTGGTGCAC 60
Db      1613 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCATTTGGTGGTGCAC 1672

QY      61 CTC 63
Db      1673 CTC 1675

RESULT 43
US-09-479-123-28
; Sequence 28, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-28

Query Match      100.0%; Score 63; DB 4; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTAAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCATTTGGTGGTGCAC 60
Db      1613 TTAAAGTGGCTAGCTCGATACATAAAGCCATTGGACCATTCACCATTTGGTGGTGCAC 1672

QY      61 CTC 63
Db      1673 CTC 1675

RESULT 43
US-09-479-123-28
; Sequence 28, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-24

Query Match      100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTAAGTGCCTAGCTCGATACATAAAGCCATTGGACATTTCACCATTCGCTGTGCAC 60
Db      1747  TTTAAGTGCCTAGCTCGATACATAAAGCCATTGGACATTTCACCATTCGCTGTGCAC 1806

QY      61  CTC 63
Db      1807  CTC 1809

RESULT 45
US-09-481-355-24
; Sequence 24; Application US/09481355
; Patent No. 6524824
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHEPP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003F
; CURRENT APPLICATION NUMBER: US/09/481,355
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-355-24

Query Match      100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TTTAAGTGCCTAGCTCGATACATAAAGCCATTTCACCATTCGCTGTGCAC 60
Db      1747  TTTAAGTGCCTAGCTCGATACATAAAGCCATTTCACCATTCGCTGTGCAC 1806

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QY 61 CTC 63
|||
Db 1807 CTC 1809

RESULT 46

US-09-481-282-24
; Sequence 24, Application US/09481282
; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003US
; CURRENT APPLICATION NUMBER: US/09/481,282
; CURRENT FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-481-282-24

Query Match 100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 1747 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1806

QY 61 CTC 63
|||
Db 1807 CTC 1809

RESULT 47

US-09-455-659A-24
; Sequence 24, Application US/09455659A
; Patent No. 6602686
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003A
; CURRENT APPLICATION NUMBER: US/09/455,659A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-455-659A-24

Query Match 100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1747 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1806
QY 61 CTC 63
|||
Db 1807 CTC 1809

RESULT 48

US-09-484-996-24
; Sequence 24, Application US/09484996
; Patent No. 6623958
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003H
; CURRENT APPLICATION NUMBER: US/09/484,996
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1998-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-996-24

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Query Match      100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 60
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Db 1747 TTTAAGTGCTAGCTCGATACATAAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 1806

QY 61 CTC 63
|||
Db 1807 CTC 1809

RESULT 49
US-09-479-123-24
; Sequence 24, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8491)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-24

Query Match      100.0%; Score 63; DB 4; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1747 TTTAAGTGCTAGCTCGATACATAAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 1806

QY 61 CTC 63
|||
Db 1807 CTC 1809

RESULT 50
US-09-479-122-25
; Sequence 25, Application US/09479122
; Patent No. 6410266
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-25

Query Match      100.0%; Score 63; DB 4; Length 10060;
Best Local Similarity 100.0%; Pred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATACATAAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 60
|||||
Db 1936 TTTAAGTGCTAGCTCGATACATAAAAGCCATTGGACCATTCACCAATTGGTGTGCAC 1995

QY 61 CTC 63
|||
Db 1996 CTC 1998

RESULT 51
US-09-484-997-25
; Sequence 25, Application US/09484997
; Patent No. 6524818
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERP, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003J
; CURRENT APPLICATION NUMBER: US/09/484,997
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-122-25
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; OTHER INFORMATION: a, c, t, g, other or unknown
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-484-997-25

Query Match 100.0%; Score 63; DB 4; Length 10060;

Best Local Similarity 100.0%; Pred. No. 6.1e-15;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
DB 1936 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1995
|||||

QY 61 CTC 63

DB 1996 CTC 1998

RESULT 52

US-09-481-355-25

; Sequence 25, Application US/09481355

; Patent No. 6524824

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE REFERENCE: 0221-0003F

; CURRENT APPLICATION NUMBER: US/09/481,355

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 10060

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURES:

; NAME/KEY: modified_base

; LOCATION: (8670)

; OTHER INFORMATION: a, c, t, g, other or unknown

; NAME/KEY: modified_base

; LOCATION: (8822)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-09-481-355-25

Query Match 100.0%; Score 63; DB 4; Length 10060;

Best Local Similarity 100.0%; Pred. No. 6.1e-15;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
DB 1936 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1995
|||||

QY 61 CTC 63

DB 1996 CTC 1998

RESULT 53

US-09-481-282-25

; Sequence 25, Application US/09481282

; Patent No. 6541221
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE REFERENCE: 0221-0003US

; CURRENT APPLICATION NUMBER: US/09/481,282

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 10060

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURES:

; NAME/KEY: modified_base

; LOCATION: (8670)

; OTHER INFORMATION: a, c, t, g, other or unknown

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (8822)

; OTHER INFORMATION: a, c, t, g, other or unknown

US-09-481-282-25

Query Match 100.0%; Score 63; DB 4; Length 10060;

Best Local Similarity 100.0%; Pred. No. 6.1e-15;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
DB 1936 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1995
|||||

QY 61 CTC 63

DB 1996 CTC 1998

RESULT 54

US-09-455-659A-25

; Sequence 25, Application US/09455659A

; Patent No. 6602686

; GENERAL INFORMATION:

; APPLICANT: HARRINGTON, JOHN J.

; APPLICANT: SHERF, BRUCE

; APPLICANT: RUNDLETT, STEPHEN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF

; FILE REFERENCE: 0221-0003A

; CURRENT APPLICATION NUMBER: US/09/455,659A

; PRIOR FILING DATE: 1999-12-07

; PRIOR APPLICATION NUMBER: 09/276,820

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/263,814

; PRIOR FILING DATE: 1999-03-08

; PRIOR APPLICATION NUMBER: 09/253,022

; PRIOR FILING DATE: 1999-02-19

; PRIOR APPLICATION NUMBER: 09/159,643

; PRIOR FILING DATE: 1998-09-24

; PRIOR APPLICATION NUMBER: 08/941,223

; PRIOR FILING DATE: 1997-09-26

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

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Db      1996 CTC 1998      |||
RESULT 56
US-09-479-123-25
; Sequence 25, Application US/09479123
; Patent No. 6670185
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDELTT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003B
; CURRENT APPLICATION NUMBER: US/09/479,123
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-09-479-123-25
Query Match      100.0%; Score 63; DB 4; Length 10060;
Best Local Similarity 100.0%; Fred. No. 6.1e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTCGGTGTGCAC 60
Db      1936 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACACATTCGGTGTGCAC 1995
QY      61 CTC 63      |||
Db      1996 CTC 1998
RESULT 57
US-09-167-322-13
; Sequence 13, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; APPLICANT: England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCE: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/167,322
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-167-322-13

Query Match          98.4%  Score 62;  DB 4;  Length 565;
Best Local Similarity 100.0%;  Pred. No. 7.5e-15;
Matches 62;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 1 TTTAAGTCCTAGCTGATACATAAAGCGCATTTGACCAATTCACCAATGTTGTGCAC 60
Db 439 TTTAAGTCCTAGCTGATACATAAAGCGCATTTGACCAATTCACCAATGTTGTGCAC 498

QY 61 CT 62
Db 499 CT 500

RESULT 58
US-09-470-881-1
; Sequence 1, Application US/09470881
; Patent No. 6685938
; GENERAL INFORMATION:
; APPLICANT: ELICHEIRI, Brian
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
; TITLE OF INVENTION: ANGIOGENESIS AND VASCULAR PERMEABILITY USING SRC OR
; TITLE OF INVENTION: YES TYROSINE KINASES
; FILE REFERENCE: T891 651.2
; CURRENT APPLICATION NUMBER: US/09/470,881
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US99/11780
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,220
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 11627
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: RCASBP(A) based
; OTHER INFORMATION: on avian sarcoma virus
; NAME/KEY: misc feature
; LOCATION: (7649)..(11258)
; OTHER INFORMATION: pBR322 sequences
; NAME/KEY: LTR
; LOCATION: (7166)..(7494)
; OTHER INFORMATION: upstream
; NAME/KEY: LTR
; LOCATION: (1)..(101)

; OTHER INFORMATION: upstream (numbering begins at the upstream R)
; NAME/KEY: misc feature
; LOCATION: (11394)..(11623)
; OTHER INFORMATION: U3
; NAME/KEY: misc feature
; LOCATION: (1)..(21)
; OTHER INFORMATION: R
; NAME/KEY: misc feature
; LOCATION: (22)..(101)
; OTHER INFORMATION: U5
; NAME/KEY: misc feature
; LOCATION: (102)..(119)
; NAME/KEY: LTR
; LOCATION: (7166)..(7494)
; OTHER INFORMATION: downstream
; NAME/KEY: misc feature
; LOCATION: (7166)..(7393)
; OTHER INFORMATION: U3
; NAME/KEY: misc feature
; LOCATION: (7394)..(7414)
; OTHER INFORMATION: R
; NAME/KEY: misc feature
; LOCATION: (7415)..(7494)
; OTHER INFORMATION: U5
; NAME/KEY: misc feature
; LOCATION: (7154)..(7165)
; OTHER INFORMATION: PPT
; NAME/KEY: misc feature
; LOCATION: (388)..(391)
; OTHER INFORMATION: splice donor (AGGT)
; NAME/KEY: misc feature
; LOCATION: (5074)..(5077)
; OTHER INFORMATION: env splice acceptor (AGGC)
; NAME/KEY: misc feature
; LOCATION: (6982)..(6985)
; OTHER INFORMATION: C1a1 splice acceptor (AGGA)
; NAME/KEY: gene
; LOCATION: (372)..(902)
; OTHER INFORMATION: gag p19
; NAME/KEY: gene
; LOCATION: (909)..(1094)
; OTHER INFORMATION: gag p10
; NAME/KEY: gene
; LOCATION: (1095)..(1814)
; OTHER INFORMATION: gag p27
; NAME/KEY: gene
; LOCATION: (1843)..(2108)
; OTHER INFORMATION: gag p12
; NAME/KEY: gene
; LOCATION: (2109)..(2480)
; OTHER INFORMATION: gag p15
; NAME/KEY: misc signal
; LOCATION: (2481)..(2483)
; OTHER INFORMATION: gag stop
; NAME/KEY: gene
; LOCATION: (2501)..(4216)
; OTHER INFORMATION: pol Rt
; NAME/KEY: gene
; LOCATION: (4217)..(5185)
; OTHER INFORMATION: pol IN
; NAME/KEY: misc signal
; LOCATION: (5186)..(5188)
; OTHER INFORMATION: pol stop
; NAME/KEY: gene
; LOCATION: (5244)..(6263)
; OTHER INFORMATION: env gp85
; NAME/KEY: gene
; LOCATION: (6264)..(6878)
; OTHER INFORMATION: env gp37
; NAME/KEY: misc signal
; LOCATION: (6879)..(6881)
; OTHER INFORMATION: env stop
; NAME/KEY: misc feature
```

```
; LOCATION: (7027)
; OTHER INFORMATION: ClaI site/ the ClaI site in gag is methylated in
; OTHER INFORMATION: Dam+ strains and does not cut
US-09-470-881-1

Query Match          98.4%; Score 62; DB 4; Length 11627;
Best Local Similarity 100.0%; Pred. No. 1.5e-14; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
Db 7367 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60

QY 61 CTC 62
Db 7427 CT 7428

RESULT 59
US-08-564-313-1
; Sequence 1, Application US/08564313
; Patent No. 5910488
; GENERAL INFORMATION:
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,313
; FILING DATE: 01-DEC-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033CP1
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; IMMEDIATE SOURCE:
; CLONE: HLA-B7 and Beta-2
US-08-564-313-1

Query Match          92.4%; Score 58.2; DB 2; Length 4965;
Best Local Similarity 95.2%; Pred. No. 3.7e-13;
Matches 60; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
Db 461 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 520

QY 61 CTC 63
Db 521 CTC 523

RESULT 60
PCT-US94-06069-1
; Sequence 1, Application PC/TUS9406069
; GENERAL INFORMATION:
; APPLICANT: Vical Incorporated
; APPLICANT: Regents of the University of Michigan
; APPLICANT: Nabel, Elizabeth
; APPLICANT: Nabel, Gary
; APPLICANT: Lew, Denise
; APPLICANT: Marquet, Magda
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06069
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/074,344
; FILING DATE: 07-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: VICAL.033VPC
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN: HLA-B7 and Beta-2
PCT-US94-06069-1

Query Match          92.4%; Score 58.2; DB 5; Length 4965;
Best Local Similarity 95.2%; Pred. No. 3.7e-13;
Matches 60; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 60
Db 461 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCAATTCACCAATGGTGTGCAC 520

QY 61 CTC 63
Db 521 CTC 523
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Db 521 CTC 523

RESULT 61

US-08-272-513-1
; Sequence 1, Application US/08272513
; Patent No. 5558867
; GENERAL INFORMATION:
; APPLICANT: Sakaguchi, Masaaki
; APPLICANT: Yamamoto, Michitaka
; TITLE OF INVENTION: RECOMBINANT MAREK'S DISEASE VIRUS,
; TITLE OF INVENTION: PROCESS FOR PREPARING THE SAME AND VACCINE CONTAINING THE
; TITLE OF INVENTION: SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wegner, Cantor, Mueller & Player
; STREET: 1233 20th Street, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20036-8218
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,513
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,554
; FILING DATE: 08-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P-500-23477
; TELEPHONE: 202-887-0400
; TELEFAX: 202-835-0605
; TELEX: 440706
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3001 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Marek's disease gammaherpesvirus
; STRAIN: 61-554 and BC-1
US-08-272-513-1

Query Match 67.9%; Score 42.8; DB 1; Length 3001;
Best Local Similarity 80.6%; Pred. No. 3e-07;
Matches 50; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 TTTAAGTCCTAGTCGATACATAAAGCCGCAATTCACCATTCACCATTCGTTGTCAC 60
Db 2110 TATAAGCTGTGGCCACCATCAATAAAGCCGCAATTCACCATTCGTTGTCAC 2169

QY 61 CT 62

Db 2170 CT 2171

RESULT 62

US-08-379-452-9/C
; Sequence 9, Application US/08379452
; Patent No. 6040174
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANI, Andrea

; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; TITLE OF INVENTION: COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWICKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,452
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
US-08-379-452-9

Query Match 52.4%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 30 CCATTTCACCATTCACCATTCGTTGTCACCT 62
Db 47 CCATTTCACCATTCACCATTCGTTGTCACCT 15

RESULT 63

US-08-682-794-5/C
; Sequence 5, Application US/08682794
; Patent No. 6110735
; GENERAL INFORMATION:
; APPLICANT: Ccile CHARTIER et al.
; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
; TITLE OF INVENTION: HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/08/682,794
; CURRENT FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-08-682-794-5

Query Match 52.4%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CCATTGACCAATTCACCAATGGTGACCT 62
Db 47 CCATTGACCAATTCACCAATGGTGACCT 15

RESULT 64
US-09-409-670-9/c
; Sequence 9, Application US/09409670
; Patent No. 6133028
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/409,670
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,452
; FILING DATE: 26-JAN-1995
; APPLICATION NUMBER: WO PCT/FR94/00624
; FILING DATE: 27-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93 06482
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadlo, Susan M.
; REGISTRATION NUMBER: 40,373
; REFERENCE/DOCKET NUMBER: 029395-002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; ORGANISM: Synthetic oligonucleotide (OTG5893)
US-09-409-670-9

Query Match 52.4%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CCATTGACCAATTCACCAATGGTGACCT 62
Db 47 CCATTGACCAATTCACCAATGGTGACCT 15

RESULT 65
US-09-467-952-5/c
; Sequence 5, Application US/09467952
; Patent No. 6281000
; GENERAL INFORMATION:
; APPLICANT: Ccile CHARTIER et al.

; TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
; FILE REFERENCE: 032751-002
; CURRENT APPLICATION NUMBER: US/09/467,952
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 08/682,794
; EARLIER FILING DATE: 1996-08-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 47
; TYPE: DNA
; ORGANISM: rous sarcoma virus
US-09-467-952-5

Query Match 52.4%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CCATTGACCAATTCACCAATGGTGACCT 62
Db 47 CCATTGACCAATTCACCAATGGTGACCT 15

RESULT 66
US-08-989-394-10
; Sequence 10, Application US/08989394
; Patent No. 5994136
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Fareson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,394
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-989-394-10

Query Match 46.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACATAAAG 29

Db 27 TTTAAGTCCTAGCTCGATACATAAAGC 55
|||||

RESULT 67
US-08-989-394-11/c
; Sequence 11, Application US/08989394
; Patent No. 5994136
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,394
FILING DATE: 12-DEC-1997

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-989-394-11
Query Match 46.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTAAGTCCTAGCTCGATACATAAAGC 29
Db 52 TTTAAGTCCTAGCTCGATACATAAAGC 24
|||||

RESULT 68
US-09-271-365-10
; Sequence 10, Application US/09271365
; Patent No. 6165782
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle

TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington

US-09-271-365-10
Query Match 46.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTAAGTCCTAGCTCGATACATAAAGC 29
Db 52 TTTAAGTCCTAGCTCGATACATAAAGC 24
|||||

STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997

ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-09-271-365-10
Query Match 46.0%; Score 29; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTAAGTCCTAGCTCGATACATAAAGC 29
Db 27 TTTAAGTCCTAGCTCGATACATAAAGC 55
|||||

RESULT 69
US-09-271-365-11/c
; Sequence 11, Application US/09271365
; Patent No. 6165782
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/271,365
FILING DATE: 18-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/989,394
FILING DATE: 12-DEC-1997
ATTORNEY/AGENT INFORMATION:

NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: A7086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-271-365-11

Query Match 46.0%; Score 29; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGC 29
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Db 52 TTTAAGTCCTAGCTCGATACATAAAGC 24
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RESULT 70
US-09-604-013A-10
; Sequence 10, Application US/09604013A
; Patent No. 6428953
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; Parson, Deborah A.
; Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/604,013A
; FILING DATE: 26-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-604-013A-10

Query Match 46.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 27 TTTAAGTCCTAGCTCGATACATAAAGC 55
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RESULT 71
US-09-604-013A-11/c
; Sequence 11, Application US/09604013A
; Patent No. 6428953
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; Parson, Deborah A.
; Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/604,013A
; FILING DATE: 26-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-604-013A-11

Query Match 46.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGC 29
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Db 52 TTTAAGTCCTAGCTCGATACATAAAGC 24
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RESULT 72
US-09-167-322-10
; Sequence 10, Application US/09167322

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; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-167-322-10
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; RESULT 73
US-08-404-531B-19
; Sequence 19, Application US/08404531B
; Patent No. 5863724
; GENERAL INFORMATION:
; APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
; APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
; TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonyleurea Receptor
; Patent No. 5863724
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5863724ris
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/404,531B
; FILING DATE: 15-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-404-531B-19
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Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TTGACCATTCACACATTTGGTGTGC 25
;
; RESULT 74
US-08-476-900A-19
; Sequence 19, Application US/08476900A
; Patent No. 6031150
; GENERAL INFORMATION:
; APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson
; TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonyleurea Receptor
; Patent No. 6031150
; TITLE OF INVENTION: and Method of Detecting Persistent Hyperinsulinemic Hypoglycemia
; TITLE OF INVENTION: Infancy
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6031150ris
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,900A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-476-900A-19

Query Match 39.7%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTGACCATTCACCACTGGTGTGC 25

RESULT 75
US-08-488-546A-19
; Sequence 19, Application US/08488546A
; Patent No. 6054313
; GENERAL INFORMATION:
; APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
; APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
; TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonyleurea Receptor
; Patent No. 6054313
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6054313ris
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,531
; FILING DATE: 15-MARCH-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardsell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-488-546A-19

Query Match 39.7%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TTGACCATTCACCACTGGTGTGC 58
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Db 1 TTGACCATTCACCACTGGTGTGC 25

Search completed: March 11, 2004, 11:10:02

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 08:24:22 ; Search time 45.7306 Seconds
(without alignments)
5071.893 Million cell updates/sec

Title: US-09-733-368A-1_COPY_550_612

Perfect score: 63
Sequence: 1 ttttaagtcctagctcgata.....accacattggtgcacctc 63

Scoring table: IDENTITY NUC

Gapc 10.0 , Gapext 1.0

Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 100 summaries

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	63	100.0	7492	14	US-10-267-117-5
3	63	100.0	7492	14	US-10-340-112-5
4	63	100.0	8238	10	US-09-482-682-50
5	63	100.0	8902	9	US-09-728-416A-1
6	63	100.0	9737	14	US-10-331-329-22
7	63	100.0	9737	14	US-10-331-329-23
8	63	100.0	9737	14	US-10-331-329-28
9	63	100.0	9871	14	US-10-331-329-24
10	63	100.0	10060	14	US-10-331-329-25
11	63	100.0	11265	14	US-10-185-318-1
12	63	100.0	11265	14	US-10-185-799-1
13	63	100.0	11600	9	US-09-847-101B-35
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Sequence 43, Appl	19	63	100.0	35211	15	US-10-403-337-43	Sequence 43, Appl
Sequence 43, Appl	20	63	100.0	35211	15	US-10-351-890-43	Sequence 43, Appl
Sequence 69, Appl	21	60.4	95.9	262	9	US-09-965-703-69	Sequence 69, Appl
Sequence 61, Appl	22	60.4	95.9	262	12	US-10-239-134-61	Sequence 61, Appl
Sequence 63, Appl	23	60.4	95.9	766	15	US-10-264-237-633	Sequence 63, Appl
Sequence 36, Appl	24	60.4	95.9	5283	11	US-09-921-143-36	Sequence 36, Appl
Sequence 9, Appl	25	46.8	74.3	5130	9	US-09-897-006-9	Sequence 9, Appl
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Sequence 9, Appl	27	33	52.4	47	9	US-09-725-720-9	Sequence 9, Appl
Sequence 5, Appl	28	33	52.4	47	9	US-09-938-431-5	Sequence 5, Appl
Sequence 9, Appl	29	33	52.4	47	10	US-09-739-007-9	Sequence 9, Appl
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Sequence 43374, A	35	23.8	37.8	328	12	US-10-424-599-43374	Sequence 43374, A
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Sequence 37698, Ap	40	23.8	37.8	738	15	US-10-369-493-37698	Sequence 37698, Ap
Sequence 1335, Ap	41	23.8	37.8	759	15	US-10-012-697-1335	Sequence 1335, Ap
Sequence 206869, A	42	23.6	37.5	594	15	US-10-027-632-206869	Sequence 206869, A
Sequence 3677, Ap	43	23.6	37.5	1174	9	US-09-938-842A-3677	Sequence 3677, Ap
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Sequence 56424, A	45	23.4	37.1	469	15	US-10-027-632-56424	Sequence 56424, A
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Sequence 226287, A	47	23.4	37.1	640	15	US-10-027-632-226287	Sequence 226287, A
Sequence 3211, Ap	48	23.4	37.1	701	15	US-10-027-632-3211	Sequence 3211, Ap
Sequence 19327, A	49	23.2	36.8	819	12	US-10-282-122A-19327	Sequence 19327, A
Sequence 165752, A	50	23.2	36.8	834	15	US-10-027-632-165752	Sequence 165752, A
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Sequence 459, App	53	23	36.5	644	14	US-10-031-504-459	Sequence 459, App
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Sequence 311371, A	68	22.4	35.6	433	15	US-10-027-632-311371	Sequence 311371, A
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Sequence 3, Appl	83	22.4	35.6	1488	14	US-10-305-633-1	Sequence 3, Appl
Sequence 3, Appl	84	22.4	35.6	1488	14	US-10-305-633-3	Sequence 3, Appl
Sequence 197, App	85	22.4	35.6	2848	9	US-09-938-980-197	Sequence 197, App
Sequence 49, Appl	86	22.4	35.6	7945	14	US-10-138-098-49	Sequence 49, Appl
Sequence 51, Appl	87	22.4	35.6	9326	14	US-10-138-701-51	Sequence 51, Appl
Sequence 23, Appl	88	22.4	35.6	17310	8	US-08-781-986A-23	Sequence 23, Appl

89 22.4 35.6 17310 12 US-10-329-624-23 Sequence 23, Appl
 c 90 22.4 35.6 32064 15 US-10-158-034-117 Sequence 117, App
 c 91 22.4 35.6 32373 9 US-09-776-705-3 Appli
 92 22.2 35.2 305 12 US-10-424-599-28157 Sequence 3, Appli
 93 22.2 35.2 822 15 US-10-369-493-23964 Sequence 28157, A
 c 94 22.2 35.2 5139 9 US-09-764-869-1894 Sequence 23964, A
 c 95 22.2 35.2 5139 14 US-10-091-504-1894 Sequence 1894, Ap
 c 96 22.2 35.2 5139 15 US-10-227-577-1894 Sequence 1894, Ap
 c 97 22.2 35.2 8697 12 US-10-158-844-123 Sequence 123, App
 c 98 22.2 35.2 78056 13 US-10-109-551-1 Sequence 1, Appli
 c 99 22 34.9 39 10 US-09-996-073-28 Sequence 28, Appl
 c 100 22 34.9 411 9 US-09-864-761-17008 Sequence 17008, A

ALIGNMENTS

RESULT 1
 US-10-331-329-18
 ; Sequence 18, Application US/10331329
 ; Publication No. US20030180267A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HARRINGTON, JOHN J.
 ; APPLICANT: SHERP, BRUCE
 ; APPLICANT: RUNDLETT, STEPHEN
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
 ; TITLE OF INVENTION: ENDOGENOUS GENES
 ; FILE REFERENCE: 0221-0003CON
 ; CURRENT APPLICATION NUMBER: US/10/331,329
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: 09/276,820
 ; PRIOR FILING DATE: 1999-03-26
 ; PRIOR APPLICATION NUMBER: 09/263,814
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: 09/253,022
 ; PRIOR FILING DATE: 1999-02-19
 ; PRIOR APPLICATION NUMBER: 09/159,643
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 08/941,223
 ; PRIOR FILING DATE: 1997-09-26
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 6836
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-331-329-18

Query Match 100.0%; Score 63; DB 14; Length 6836;
 Best Local Similarity 100.0%; Pred. No. 5.5e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 Db 1760 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 1819
 QY 61 CTC 63
 Db 1820 CTC 1822

RESULT 2
 US-10-267-117-5
 ; Sequence 5, Application US/10267117
 ; Publication No. US20030082162A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FLOTTE, TERENCE R.
 ; APPLICANT: SONG, SIHONG
 ; APPLICANT: BYRNE, BARRY J.
 ; APPLICANT: MORGAN, MICHAEL
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
 ; FILE REFERENCE: 4300.011800
 ; CURRENT APPLICATION NUMBER: US/10/267,117

; CURRENT FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: US/09/299,141
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/083,025
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-24
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 7492
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
 US-10-267-117-5

Query Match 100.0%; Score 63; DB 14; Length 7492;
 Best Local Similarity 100.0%; Pred. No. 5.7e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 Db 27 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 86
 QY 61 CTC 63
 Db 87 CTC 89

RESULT 3
 US-10-340-112-5
 ; Sequence 5, Application US/10340112
 ; Publication No. US20030095949A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FLOTTE, TERENCE R.
 ; APPLICANT: SONG, SIHONG
 ; APPLICANT: BYRNE, BARRY J.
 ; APPLICANT: MORGAN, MICHAEL
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
 ; FILE REFERENCE: 4300.011800
 ; CURRENT APPLICATION NUMBER: US/10/340,112
 ; CURRENT FILING DATE: 2003-01-10
 ; PRIOR APPLICATION NUMBER: US/09/299,141
 ; PRIOR FILING DATE: 1999-04-23
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/083,025
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-24
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 7492
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:p43C-AT-IN
 US-10-340-112-5

Query Match 100.0%; Score 63; DB 14; Length 7492;
 Best Local Similarity 100.0%; Pred. No. 5.7e-14;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
 Db 27 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 86
 QY 61 CTC 63
 Db 87 CTC 89

RESULT 4
 US-09-482-682-50
 ; Sequence 50, Application US/09482682
 ; Publication No. US20030157688A1
 ; GENERAL INFORMATION:

```
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 8238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-50

Query Match      100.0%; Score 63; DB 10; Length 8238;
Best Local Similarity 100.0%; Pred. No. 5.8e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
    |||||
Db 742 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 801
    |||||

Qy 61 CTC 63
    |||
Db 802 CTC 804

RESULT 5
US-09-729-416A-1
; Sequence 1, Application US/03729416A
; Patent No. US20020055172A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; TITLE OF INVENTION: MULTIPLE PROMOTER EXPRESSION CONSTRUCTS AND METHODS OF
; FILE REFERENCE: 0221-0004C
; CURRENT APPLICATION NUMBER: US/09/729,416A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8902
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-729-416A-1

Query Match      100.0%; Score 63; DB 9; Length 8902;
Best Local Similarity 100.0%; Pred. No. 6e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
    |||||
Db 3826 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 3885
    |||||

Qy 61 CTC 63
    |||
Db 3886 CTC 3888

RESULT 6
US-10-331-329-22
; Sequence 22, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
```

```
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-22

Query Match      100.0%; Score 63; DB 14; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 60
    |||||
Db 1613 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGGCAC 1672
    |||||

Qy 61 CTC 63
    |||
Db 1673 CTC 1675

RESULT 7
US-10-331-329-23
; Sequence 23, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT APPLICATION NUMBER: US/10/331,329
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
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; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-23

Query Match      100.0%; Score 63; DB 14; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 1613 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1672

QY 61 CTC 63
Db 1673 CTC 1675

RESULT 8
US-10-331-329-28
; Sequence 28, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT FILING DATE: 2002-12-30
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9737
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8347)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8499)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-28

Query Match      100.0%; Score 63; DB 14; Length 9737;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 1613 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1672

QY 61 CTC 63
Db 1673 CTC 1675

RESULT 9
US-10-331-329-24
; Sequence 24, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT FILING DATE: 2002-12-30
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 9871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8481)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8633)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-24

Query Match      100.0%; Score 63; DB 14; Length 9871;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
Db 1747 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1805

QY 61 CTC 63
Db 1807 CTC 1809

RESULT 10
US-10-331-329-25
; Sequence 25, Application US/10331329
; Publication No. US20030180267A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; FILE REFERENCE: 0221-0003CON
; CURRENT FILING DATE: 2002-12-30
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/276,820
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 09/263,814

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; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 10060
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8670)
; OTHER INFORMATION: a, c, t, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8822)
; OTHER INFORMATION: a, c, t, g, other or unknown
US-10-331-329-25
Query Match 100.0%; Score 63; DB 14; Length 10060;
Best Local Similarity 100.0%; Pred. No. 6.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
Db 1936 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 1995
QY 61 CTC 63
|||
Db 1996 CTC 1998

RESULT 11
US-10-185-318-1
; Sequence 1, Application US/10185318
; Publication No. US20030035793A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, JEFFREY S.
; APPLICANT: BRADY, JAMIE L.
; APPLICANT: LEW, ANDREW M.
; TITLE OF INVENTION: NOVEL IMMUNE RESPONSE TARGETING MOLECULES
; FILE REFERENCE: FBRC:009USC2
; CURRENT APPLICATION NUMBER: US/10/185,318
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/402,020
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: PCT/AU98/00208
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: AU PP5891
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: AU PP1830
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11265
; TYPE: DNA
; ORGANISM: Murine
US-10-185-318-1

Query Match 100.0%; Score 63; DB 14; Length 11265;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
Db 571 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 630
QY 61 CTC 63

Db 631 CTC 633
|||
RESULT 12
US-10-185-799-1
; Sequence 1, Application US/10185799
; Publication No. US2003007242A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, JEFFREY S.
; APPLICANT: BRADY, JAMIE L.
; APPLICANT: LEW, ANDREW M.
; TITLE OF INVENTION: ENHANCEMENT OF IMMUNE RESPONSE USING TARGETING
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: FBRC:009USC1
; CURRENT APPLICATION NUMBER: US/10/185,799
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 09/402,020
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: PCT/AU98/00208
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: AU PP5891
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: AU PP1830
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11265
; TYPE: DNA
; ORGANISM: Murine
US-10-185-799-1

Query Match 100.0%; Score 63; DB 14; Length 11265;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
|||||
Db 571 TTTAAGTGCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 630
QY 61 CTC 63
|||
Db 631 CTC 633

RESULT 13
US-09-847-101B-35
; Sequence 35, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: FRIEDLANDER, MARTIN
; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THERAPY
; FILE REFERENCE: 22908-1226B
; CURRENT APPLICATION NUMBER: US/09/847,101B
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/562,934
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid MMTV-E2a-SV40-Neo
US-09-847-101B-35

Query Match 100.0%; Score 63; DB 9; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86

QY 61 CTC 63
Db 87 CTC 89

RESULT 14
US-09-482-682-49
; Sequence 49, Application US/09482682
; Publication No. US20030157688A1
; GENERAL INFORMATION:
; APPLICANT: VON SEGGERN, DANIEL
; APPLICANT: NEMEROW, GLEN R.
; APPLICANT: HALLENBECK, PAUL
; APPLICANT: STEVENSON, SUSAN
; APPLICANT: SKRIPCHENKO, YELENA
; TITLE OF INVENTION: ADENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
; AND METHODS FOR PREPARATION AND USE
; FILE REFERENCE: 1294.0010001
; CURRENT APPLICATION NUMBER: US/09/482,682
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-482-682-49

Query Match 100.0%; Score 63; DB 10; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86

QY 61 CTC 63
Db 87 CTC 89

RESULT 15
US-10-403-337-42
; Sequence 42, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-10-403-337-42

Query Match 100.0%; Score 63; DB 10; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86

QY 61 CTC 63
Db 87 CTC 89

RESULT 16
US-10-351-890-42
; Sequence 42, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Nco
US-10-351-890-42

Query Match 100.0%; Score 63; DB 15; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86

QY 61 CTC 63
Db 87 CTC 89

RESULT 17
US-10-403-337-44
; Sequence 44, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Nco
US-10-403-337-42

Query Match 100.0%; Score 63; DB 15; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86

QY 61 CTC 63
Db 87 CTC 89

RESULT 18
US-10-351-890-42
; Sequence 42, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid MMTV-E2a-SV40-Nco
US-10-351-890-42

Query Match 100.0%; Score 63; DB 15; Length 11600;
Best Local Similarity 100.0%; Pred. No. 6.5e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 60
Db 27 TTTAAGTCCTAGCTCGATACATAAAGCGCATTTGACCAATTCACCAATTTGGTGTGCAC 86

QY 61 CTC 63
Db 87 CTC 89

RESULT 19
US-10-403-337-44
; Sequence 44, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 42
; LENGTH: 11600
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```

; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 33622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av3nBg
US-10-403-337-44

Query Match          100.0%; Score 63; DB 15; Length 33622;
Best Local Similarity 100.0%; Pred. No. 9.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 734 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 793

QY 61 CTC 63
    |||
Db 794 CTC 796

RESULT 18
US-10-351-890-44
; Sequence 44, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 33622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av3nBg
US-10-351-890-44

Query Match          100.0%; Score 63; DB 15; Length 33622;
Best Local Similarity 100.0%; Pred. No. 9.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 734 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 793

QY 61 CTC 63
    |||
Db 794 CTC 796

RESULT 19
US-10-403-337-43
; Sequence 43, Application US/10403337
; Publication No. US20030215948A1
; GENERAL INFORMATION:
; APPLICANT: Kaleko, Michael
; APPLICANT: Nemerow, Glen R.

```

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; APPLICANT: Smith, Theodore
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236B
; CURRENT APPLICATION NUMBER: US/10/403,337
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 10/351,890
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 35211
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av1nBg
US-10-403-337-43

Query Match          100.0%; Score 63; DB 15; Length 35211;
Best Local Similarity 100.0%; Pred. No. 9.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 848 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 907

QY 61 CTC 63
    |||
Db 908 CTC 910

RESULT 20
US-10-351-890-43
; Sequence 43, Application US/10351890
; Publication No. US20040002060A1
; GENERAL INFORMATION:
; APPLICANT: Stevenson, Susan C.
; APPLICANT: Kaleko, Michael
; APPLICANT: Smith, Theodore
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: Fiber Shaft Modifications for Efficient Targeting
; FILE REFERENCE: 22908-1236
; CURRENT APPLICATION NUMBER: US/10/351,890
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/350,388
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/391,967
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 35211
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid Av1nBg
US-10-351-890-43

Query Match          100.0%; Score 63; DB 15; Length 35211;
Best Local Similarity 100.0%; Pred. No. 9.3e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 60
    |||||
Db 848 TTTAAGTGGCTAGCTCGATACATAAAGCCATTGACCATTCACCATTTGGTGTGCAC 907

QY 61 CTC 63
    |||
Db 908 CTC 910

```

RESULT 21

US-09-965-703-69
; Sequence 69, Application US/09965703
; Patent No. US20020119521A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20020119521A1el Ecdysone Receptor-Based Inducible Gene Expression
; FILE REFERENCE: A01020B
; CURRENT APPLICATION NUMBER: US/09/965,703
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/09050
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Rous sarcoma virus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20020119521A1el Sequence
US-09-965-703-69

Query Match 95.9%; Score 60.4; DB 9; Length 262;

Best Local Similarity 98.4%; Pred. No. 2e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGGTGCAC 60
|||||
Db 201 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGGTGCAC 260
61 CT 62
261 CT 262

RESULT 22

US-10-239-134-61
; Sequence 61, Application US/10239134
; Publication No. US20040033600A1
; GENERAL INFORMATION:
; APPLICANT: Rohm and Haas Company
; APPLICANT: Palli, Subba Reddy
; APPLICANT: Kapitskaya, Marianna Zinovjevna
; APPLICANT: Cress, Dean Ervin
; TITLE OF INVENTION: No. US20040033600A1el Ecdysone Receptor-Based Inducible Gene Expression
; FILE REFERENCE: RH0020
; CURRENT APPLICATION NUMBER: US/10/239,134
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/191,355
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/269,799
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20040033600A1el Sequence
US-10-239-134-61

Query Match 95.9%; Score 60.4; DB 12; Length 262;
Best Local Similarity 98.4%; Pred. No. 2e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGGTGCAC 60
|||||
Db 201 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGGTGCAC 260
61 CT 62
261 CT 262

RESULT 23

US-10-264-237-633
; Sequence 633, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 633
; LENGTH: 766
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (56)..(56)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (91)..(91)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (141)..(141)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (652)..(652)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (753)..(753)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (763)..(763)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-633

Query Match 95.9%; Score 60.4; DB 15; Length 766;

Best Local Similarity 98.4%; Pred. No. 2.8e-13;
Matches 61; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTAAGTCCTAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGGTGCAC 60
|||||
Db 169 TTTAAGTCCAGCTCGATACATAAAGCCATTGACCATTCACCATTCACCATTCGATGGTGCAC 228
61 CT 62
229 CT 230

RESULT 24

```

; APPLICANT: Miller, Linda
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
; FILE REFERENCE: GALA-06416
; CURRENT APPLICATION NUMBER: US/09/897,511A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,925
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 5130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-511A-9

Query Match          74.3%;   Score 46.8;   DB 10;   Length 5130;
Best Local Similarity 93.8%;   Pred. No. 9,7e-08;
Matches 60;   Conservative 0;   Mismatches 2;   Indels 2;   Gaps 1;

QY      1      TTTAAGTGCCCTAGCTCGATACATAAAGCCCA--TTTGACCACTTCACCACTTGGTGTC 58
          |||
Db      2527  TTTAAGTGCCCTAGCTCGATACAGAAAGCCCACTTTTGACCACTTCACCACTTGGTGTC 2586

QY      59  ACCT 62
          |||
Db      2587  ACCT 2590

```

RESULT 27
US-09-725-720-9/c
; Sequence 9, Application US/09725720
; Patent No. US20010049136A1
; GENERAL INFORMATION:
; APPLICANT: IMLER, Jean-Luc
; APPLICANT: MEHTALI, Majid
; APPLICANT: PAVIRANI, Andrea
; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
; TITLE OF INVENTION: COMPLEMENTATION LINES
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/725,720

/ SOFTWARE: Facsimile Release #1.00, Version #1.30
 /
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/725,720
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/379,452
 / FILING DATE:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: FR 93 06482
 / FILING DATE: 28-MAY-1993
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Radio, Susan M.
 / REGISTRATION NUMBER: 40,373
 / REFERENCE/DOCKET NUMBER: 029395-002
 / INFORMATION FOR SEQ ID NO: 9:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 47 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single

REFERENCE/DOCKET NUMBER: 029395-002
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 47 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

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/
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Synthetic oligonucleotide (OTG5893)
/ US-09-725-720-9

Query Match      52.4%; Score 33; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CCATTGACCATTCACCATTTGGTGTGCACCT 62
   |||||
Db 47 CCATTGACCATTCACCATTTGGTGTGCACCT 15

RESULT 28
US-09-938-491-5/c
/ Sequence 5, Application US/09938491
/ Patent No. US20020090715A1
/ GENERAL INFORMATION:
/ APPLICANT: Ccille CHARTIER et al.
/ TITLE OF INVENTION: METHOD OF PREPARING A VIRAL VECTOR BY INTERMOLECULAR
/ FILE REFERENCES: 032751-002
/ CURRENT APPLICATION NUMBER: US/09/938,491
/ PRIOR FILING DATE: 2001-08-27
/ PRIOR APPLICATION NUMBER: 08/682,794
/ PRIOR FILING DATE: 1996-08-01
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 47
/ TYPE: DNA
/ ORGANISM: rous sarcoma virus
/ US-09-938-491-5

Query Match      52.4%; Score 33; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CCATTGACCATTCACCATTTGGTGTGCACCT 62
   |||||
Db 47 CCATTGACCATTCACCATTTGGTGTGCACCT 15

RESULT 29
US-09-739-007-9/c
/ Sequence 9, Application US/09739007
/ Publication No. US20030170885A1
/ GENERAL INFORMATION:
/ APPLICANT: IMELER, Jean-Luc
/ PAVIRANI, Andrea
/ MEHTALI, Majid
/ TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING
/ COMPLEMENTATION LINES
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
/ STREET: 1737 King Street, Suite 500
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: United States
/ ZIP: 22314-2756
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/739,007
/ FILING DATE: 19-Dec-2000
```

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/
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/379,452
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: FR 93 06482
/ FILING DATE: 28-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dadio, Susan M.
/ REGISTRATION NUMBER: 40,373
/ REFERENCE/DOCKET NUMBER: 029395-002
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 47 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Synthetic oligonucleotide (OTG5893)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 9:
/ US-09-739-007-9

Query Match      52.4%; Score 33; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CCATTGACCATTCACCATTTGGTGTGCACCT 62
   |||||
Db 47 CCATTGACCATTCACCATTTGGTGTGCACCT 15

RESULT 30
US-10-192-085-10
/ Sequence 10, Application US/10192085
/ Publication No. US20020173030A1
/ GENERAL INFORMATION:
/ APPLICANT: Naidini, Luigi
/ Dull, Thomas
/ Farson, Deborah A.
/ Witt, Rochelle
/ TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
/ STREET: 2100 Pennsylvania Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/192,085
/ FILING DATE: 10-Jul-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/271,365
/ FILING DATE: 18-Mar-1999
/ APPLICATION NUMBER: 08/989,394
/ FILING DATE: 12-DEC-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Nakamura, Dean H.
/ REGISTRATION NUMBER: 33,981
/ REFERENCE/DOCKET NUMBER: A7086
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)293-7060
/ TELEFAX: (202)293-7860
```

```
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 74 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-192-085-10

Query Match          46.0%; Score 29; DB 13; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATCAATAAAG 29
    |||||
Db 27 TTTAAGTGCTAGCTCGATCAATAAAG 55

RESULT 31
US-10-192-085-11/c
; Sequence 11, Application US/10192085
; Publication No. US20020173030A1
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; Dull, Thomas
; Farson, Deborah A.
; Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SUGRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/192,085
; FILING DATE: 10-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 74 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-192-085-11

Query Match          46.0%; Score 29; DB 13; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATCAATAAAG 29
    |||||
Db 27 TTTAAGTGCTAGCTCGATCAATAAAG 55

US-10-155-736A-1
; Sequence 1, Application US/10155736A
; Publication No. US20030095948A1
; GENERAL INFORMATION:
; APPLICANT: Universit. di Torino
; TITLE OF INVENTION: Vector and methods of use for selective expression of genes in s
; FILE REFERENCE: 36019/MMM
; CURRENT APPLICATION NUMBER: US/10/155,736A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: -
; SEQ ID NO 1
; LENGTH: 10469
; TYPE: DNA
; ORGANISM: HIV-1
; US-10-155-736A-1

Query Match          46.0%; Score 29; DB 14; Length 10469;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTAAGTGCTAGCTCGATCAATAAAG 29
    |||||
Db 2420 TTTAAGTGCTAGCTCGATCAATAAAG 2448

RESULT 33
US-10-369-493-37332
; Sequence 37332, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 37332
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Pseudomonas fluorescens
; US-10-369-493-37332

Query Match          39.4%; Score 24.8; DB 15; Length 765;
Best Local Similarity 67.3%; Pred. No. 18;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 4 AAGTGCTAGCTCGATCAATAAAGCCATTGACCATTCACACATTGGTG 55
    |||||
Db 115 AAGTCTGGTGGTCGTAAACAATGGCCGTATTTACCACTGTCACATTGGTG 166

RESULT 34
US-10-424-599-110305/c
; Sequence 110305, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
```



```
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 110305
/ LENGTH: 741
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_70617C.1
US-10-424-599-110305
```

```
Query Match 38.1%; Score 24; DB 12; Length 741;
Best Local Similarity 64.3%; Pred. No. 37;
Matches 36; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
```

```
QY 1 TTAAAGTCCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTTGGTGT 56
|||||
Db 695 TTGATGGCTTAAATCAATTCAGTGAAGTCTTTCATCATTCATTCATGT 640
```

RESULT 35

```
US-10-424-599-43374
/ Sequence 43374, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 43374
/ LENGTH: 328
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_139166C.1
US-10-424-599-43374
```

```
Query Match 37.8%; Score 23.8; DB 12; Length 328;
Best Local Similarity 72.1%; Pred. No. 34;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 18 ATACATTAAGCGCATTTGACCATTCACCATTCACCATTTGGTGTGAC 60
|||||
Db 99 AGACATCGAAGCAAAATGATCATTAATCCCATTTGATGGAC 141
```

RESULT 36

```
US-10-424-599-63137/c
/ Sequence 63137, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
```

```
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 63137
/ LENGTH: 414
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_28026C.1
US-10-424-599-63137
```

```
Query Match 37.8%; Score 23.8; DB 12; Length 414;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
```

```
QY 1 TTAAAGTCCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTCACCAT 51
|||||
Db 390 TTGTGTGCATCTCTCTTAAAAAAGCGCGTTTGTCCATGCATAAAT 340
```

RESULT 37

```
US-10-027-632-245976
/ Sequence 245976, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 245976
/ LENGTH: 629
/ TYPE: DNA
/ ORGANISM: Human
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_139166C.1
US-10-027-632-245976
```

```
Query Match 37.8%; Score 23.8; DB 15; Length 629;
Best Local Similarity 72.1%; Pred. No. 42;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 2 TTAAGTCCCTAGCTCGATACATAAAGCGCATTTGACCATTCACCATTCACCA 44
|||||
Db 454 TGAAGATCCAAGCTAATTCATCAAGCTATTGTGATTCATTCACCA 496
```

RESULT 38

```
US-10-027-632-245977
/ Sequence 245977, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
```

; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 245977
 ; LENGTH: 629
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-027-632-245977

Query Match 37.8%; Score 23.8; DB 15; Length 629;
 Best Local Similarity 72.1%; Pred. No. 42;
 Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 TTAAGTCCCTAGCTGATACAAATAAGCCGATTTGACCATTCACCAATCA 44
 Db 454 TGAAGATCCAAGCTAATTTCAATCAAGCTATTGATCATCA 496

RESULT 39

US-10-012-697-1087
 ; Sequence 1087, Application US/10012697
 ; Publication No. US20030215803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Escobedo, Jaime
 ; APPLICANT: Garcia, Pablo Dominguez
 ; APPLICANT: Kassam, Altaf
 ; APPLICANT: Lamson, George
 ; APPLICANT: Scott, Beth
 ; APPLICANT: Drmanac, Radoje
 ; APPLICANT: Crkvenjakov, Radomir
 ; APPLICANT: Dickson, Mark
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Leshkowitz, Dena
 ; APPLICANT: Kita, David
 ; APPLICANT: Garcia, Veronica
 ; APPLICANT: Jones, Lee William
 ; APPLICANT: Stache-Crain, Birgit

; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
 ; FILE REFERENCE: 2300-16252
 ; CURRENT APPLICATION NUMBER: US/10/012,697
 ; PRIOR FILING DATE: 2003-01-21
 ; PRIOR APPLICATION NUMBER: 60/254,648
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: 60/275,668
 ; PRIOR FILING DATE: 2001-03-13
 ; NUMBER OF SEQ ID NOS: 1568
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1087

; LENGTH: 735
 ; TYPE: DNA

; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
 ; OTHER INFORMATION: n = A,T,C or G
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
 ; OTHER INFORMATION: n = A,T,C or G
 ; FEATURE:

; NAME/KEY: misc feature
 ; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
 ; OTHER INFORMATION: n = A,T,C or G
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
 ; OTHER INFORMATION: n = A,T,C or G
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 546_568, 624, 631, 649, 725, 731, 734
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-012-697-1087

Query Match 37.8%; Score 23.8; DB 15; Length 735;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TTAAAGTCCCTAGCTGATACAAATAAGCCGATTTGACCATTCACCAATTC 51
 Db 357 TTATCTCCCTTTCTCATAGATGCGACGAATTTGACCTTATGCTACACT 407

RESULT 40

US-10-369-493-37698/c
 ; Sequence 37698, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 37698
 ; LENGTH: 738
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas fluorescens
 US-10-369-493-37698

Query Match 37.8%; Score 23.8; DB 15; Length 738;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 13 GCTCGATACAAATAAGCCGATTTGACCATTCACCAATTCGATGCTGCACTC 63
 Db 624 GATCGGACGATAGACGCGAGTTCATCGAACAGCCCGGTGTGTCGCGC 574

RESULT 41

US-10-012-697-1335
 ; Sequence 1335, Application US/10012697
 ; Publication No. US20030215803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Escobedo, Jaime
 ; APPLICANT: Garcia, Pablo Dominguez
 ; APPLICANT: Kassam, Altaf
 ; APPLICANT: Lamson, George
 ; APPLICANT: Scott, Beth
 ; APPLICANT: Drmanac, Radoje
 ; APPLICANT: Crkvenjakov, Radomir
 ; APPLICANT: Dickson, Mark
 ; APPLICANT: Drmanac, Snezana
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Leshkowitz, Dena
 ; APPLICANT: Kita, David
 ; APPLICANT: Garcia, Veronica

Query Match 37.8%; Score 23.8; DB 15; Length 759;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```

; SEQ ID NO 3677
;
; LENGTH: 1174
;
; TYPE: DNA
;
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3677

```

```

Query Match      37.5%; Score 23.6; DB 9; Length 1174;
Best local Similarity 61.3%; Pred. No. 61;
Matches 38; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY      1 TTTAAGTCCTAGCTCGATACATATAACGCCATTGACCATTCACCACTGGTGTGCAC 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      467 TTCATGTGTAAAGTACGAAACATTAACATCATGAAACACTCGAAATATTTGTAGTAAC 526
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      61 CT 52
      |||
Db      527 TT 528

```

```

; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 3677
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3677

Query Match      37.1%; Score 23.6; DB 11; Length 1174;
Best Local Similarity 61.3%; Pred. No. 61;
Matches 38; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCGCATTTGACCATTCACCAATTCGTTGTCAC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 467 TTATGTTGTAAGTACGAAACATAAATACATCATGAAACACTCGAAATATTGTAGTAAC 526

QY 61 CT 62
Db 527 TT 528

RESULT 45
US-10-027-632-56424/c
; Sequence 56424, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56424
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-56424

Query Match      37.1%; Score 23.4; DB 15; Length 469;
Best Local Similarity 64.7%; Pred. No. 54;
Matches 33; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCGCATTTGACCATTCACCAATT 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 TTACTCCCTTCYCCATAGATGCGCAATTGACCTTATGCTACT 163

RESULT 46
US-10-027-632-293958/c
; Sequence 293958, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293958
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-293958

Query Match      37.1%; Score 23.4; DB 15; Length 469;
Best Local Similarity 64.7%; Pred. No. 54;
Matches 33; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 1 TTTAAGTGGCTAGCTCGATACATAAAGCGCATTTGACCATTCACCAATT 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 TTACTCCCTTCYCCATAGATGCGCAATTGACCTTATGCTACT 163

RESULT 47
US-10-027-632-226287
; Sequence 226287, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226287
; LENGTH: 640
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-226287

Query Match      37.1%; Score 23.4; DB 15; Length 640;

```

Best Local Similarity 63.2%; Pred. No. 60;
Matches 36; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 4 AAGTGGCTAGCTCGATCAATAAACCCATTGACCAATTCACCAATTTGGTGGAC 60
Db 142 AAATGAAAGCTGCTCAAAACCAACCACTGTGACTCTCAAAACAGTGGTGTAC 198

RESULT 48

US-10-027-632-3211
; Sequence 3211, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3211
; LENGTH: 701
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-3211

Query Match 37.1%; Score 23.4; DB 15; Length 701;
Best Local Similarity 64.7%; Pred. No. 62;
Matches 33; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

QY 1 TTAAAGTGGCTAGCTCGATCAATAAACCCATTGACCAATTCACCAAT 51
Db 482 TTACTCCCTTCVCCNATGATGCAGCAATTTGACCTTATGCTACT 532

RESULT 49

US-10-282-122A-19927
; Sequence 19927, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvekund, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITFA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19927
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Enterobacter cloacae
US-10-282-122A-19927

Query Match 36.8%; Score 23.2; DB 12; Length 819;
Best Local Similarity 65.4%; Pred. No. 77;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 4 AAGTGGCTAGCTCGATCAATAAACCCATTGACCAATTCACCAATTTGGTGG 55
Db 115 AAATCCGGTGGCTGTAACACATGCGCCCTATCACCCTGTCACATCGGTG 166

RESULT 50

US-10-027-632-165752/c
; Sequence 165752, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165752
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-165752

Query Match 36.8%; Score 23.2; DB 15; Length 834;
Best Local Similarity 65.4%; Pred. No. 78;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 TTAGTCTAGCTGCTACATTAACGCGCATTTGACCATTCACCATTTGG 53
Db 275 TTATAGCCTAGCTTAAGGATTAACCTGATTCAGTTTCACCACTCTGG 224

RESULT 51

US-10-027-632-165753/c
; Sequence 165753, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 168827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165753
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-165753

Query Match 36.8%; Score 23.2; DB 15; Length 834;
Best Local Similarity 65.4%; Pred. No. 78;
Matches 34; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 TTAGTCTAGCTGCTACATTAACGCGCATTTGACCATTCACCATTTGG 53
Db 275 TTATAGCCTAGCTTAAGGATTAACCTGATTCAGTTTCACCACTCTGG 224

RESULT 52

US-09-764-869-459/c
; Sequence 459, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 459
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (30)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (523)

; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (526)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (630)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-459

Query Match 36.5%; Score 23; DB 9; Length 644;
Best Local Similarity 65.3%; Pred. No. 86;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 14 CTCGATACATTAACGCGCATTTGACCATTCACCATTTGGTGTGCACCT 62
Db 553 CTCCTAATAATACAGACCCCTGGTCCANTCNCACATGGGCTTGCACCT 505

RESULT 53

US-10-091-504-459/c
; Sequence 459, Application US/10091504
; Publication No. US2003005908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 459
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (30)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (523)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (526)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (596)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (630)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-091-504-459

Query Match 36.5%; Score 23; DB 14; Length 644;
Best Local Similarity 65.3%; Pred. No. 86;
Matches 32; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 14 CTCGATACATTAACGCGCATTTGACCATTCACCATTTGGTGTGCACCT 62
Db 553 CTCCTAATAATACAGACCCCTGGTCCANTCNCACATGGGCTTGCACCT 505

RESULT 54

US-10-227-577-459/c
; Sequence 459, Application US/10227577
; Publication No. US20040005575A1
; GENERAL INFORMATION:

```

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115884
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-115884

Query Match 36.5%; Score 23; DB 15; Length 798;
Best Local Similarity 63.6%; Pred. No. 92; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 20;

QY 8 GCGTAGCTCGATACATAAAGCCATTTCACCATTCACCATTCGGTGTGCACCT 62
DB 101 GACTGCTAGAGAGATTAAAGCTACTGGCATTTCACCATTCGTTTGTGCT 155

RESULT 56
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 36.5%; Score 23; DB 9; Length 3309400;
Best Local Similarity 63.6%; Pred. No. 7.8e+02;
Matches 35; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

```

```
Qy 2 TTAAGTCCTAGCTGATACATTAAGGCAATTGACCAATTCACCACTTGGTGT 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1882470 TTAAGTCCTAGGCGATATAAAACACCGCTGTTGAAGTAATCAACAGCGTGT 1882416

RESULT 57
US-10-424-599-60097
; Sequence 60097, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Gao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 60097
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2527C.1
US-10-424-599-60097

Query Match 36.2%; Score 22.8; DB 12; Length 347;
Best Local Similarity 66.0%; Pred. No. 84;
Matches 33; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 13 GCTCGATCAATTAAGGCAATTGACCAATTCACCAATTCGTTGTCACCT 62
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 82 GCTTGAATAAAACCACTTTCACCAATTCGTTGTCACCT 131

RESULT 58
US-10-027-632-24941
; Sequence 24941, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24941
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24941

Query Match 36.2%; Score 22.8; DB 15; Length 605;
Best Local Similarity 79.4%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy 18 ATACAATAAAGCCCAATTGACCAATTCACCACTT 51
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114 ATCCAATAAAGTCCATTGGCCATAGACACATT 147

RESULT 59
US-10-027-632-106857/c
; Sequence 106857, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106857
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-106857

Query Match 36.2%; Score 22.8; DB 15; Length 645;
Best Local Similarity 79.4%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 18 ATACAATAAAGCCCAATTGACCAATTCACCACTT 51
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 ATCCAATAAAGTCCATTGGCCATAGACACATT 497

RESULT 60
US-10-027-632-136614/c
; Sequence 136614, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
```



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; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136614
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136614

Query Match      36.2%; Score 22.8; DB 15; Length 645;
Best Local Similarity 79.4%; Pred. No. 1e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 18 ATACATAAAGCCGCTTGGACCATTCACCAAT 51
    |||||
Db 530 ATCAATAAAGTCCATTTGGCCATAGACACATT 497
    |||||

RESULT 61
US-10-424-599-1697/c
; Sequence 1697, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 1697
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101531C.1
US-10-424-599-1697

Query Match      36.2%; Score 22.8; DB 12; Length 822;
Best Local Similarity 62.1%; Pred. No. 1.e+02;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 3 TAAGTCCCTAGCTCGATACAAATAAGCGCATTCGACATTCACCATTCGTTGTGTCAC 60
    |||||
Db 688 TAAGTACGCTGACAAATATAGGAAGTGGCCCATGATCAATACCATTCAGTTGTTCTC 631
    |||||

RESULT 62
US-10-424-599-100590
; Sequence 100590, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 100590
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(386)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_61847C.1
US-10-424-599-100590

Query Match      35.9%; Score 22.6; DB 12; Length 388;
Best Local Similarity 60.7%; Pred. No. 1e+02;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 TTTAAGTGCCTAGCTCGATACAAATAAGCGCATTCGACATTCACCATTCGTTGTGTCAC 60
    |||||
Db 160 TCTAAGGCCCGCTCAATATACATATACGCCAGTAATCCATGATATATATGAGACCGTAC 219
    |||||

QY 61 C 61
    |
Db 220 C 220

RESULT 63
US-10-311-455-1061/c
; Sequence 1061, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining
; FILE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1061
; LENGTH: 6696
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1061

Query Match      35.9%; Score 22.6; DB 14; Length 6696;
Best Local Similarity 60.7%; Pred. No. 2.6e+02;
Matches 37; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 3 TAAGTGCCTAGCTCGATACAAATAAGCGCATTCGACATTCACCATTCGTTGTGTCACCT 62
    |||||
Db 2816 TAATTTTATATATTTTCAATAAATAAATAATTCACCATTCACACATTTCTTTTACCT 2757
    |||||

QY 63 C 63
    |
Db 2756 C 2756

RESULT 64
US-10-240-485-87/c
; Sequence 87, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
```



```
; Sequence 311371, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311371
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-311371

Query Match      35.6%; Score 22.4; DB 15; Length 433;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 AAGTGGCTAGCTCGATACATAAAGCCGATTTGACCATTCACACAT 51
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 AAGTGCATAGGCTAGAGAGACGACCAAGAGACCTTACCAAT 177

RESULT 69
US-09-814-353-4354
; Sequence 4354, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4354
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-4354

Query Match      35.6%; Score 22.4; DB 15; Length 433;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 AAGTGGCTAGCTCGATACATAAAGCCGATTTGACCATTCACACAT 51
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 AAGTGCATAGGCTAGAGAGACGACCAAGAGACCTTACCAAT 177

RESULT 69
US-09-814-353-4354
; Sequence 4354, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4354
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-4354
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Query Match      35.6%; Score 22.4; DB 10; Length 501;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 14 CTCGATACATAAAGCCGATTTGACCATTCACCAATTTGGTGTGCACC 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 393 CTTGAACACAAATAAACAATTTGATCTCTCACACAATTTTGTGCATC 440

RESULT 70
US-09-814-353-10658
; Sequence 10658, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10658
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-10658

Query Match      35.6%; Score 22.4; DB 10; Length 501;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 14 CTCGATACATAAAGCCGATTTGACCATTCACCAATTTGGTGTGCACC 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 393 CTTGAACACAAATAAACAATTTGATCTCTCACACAATTTTGTGCATC 440

RESULT 71
US-10-138-701-54/c
; Sequence 54, Application US/10138701
; Publication No. US20030186364A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PB484
; CURRENT APPLICATION NUMBER: US/10/138,701
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/512,255A
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/098,964
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-05
; PRIOR APPLICATION NUMBER: PCT/ US99/19726
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
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; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-138-701-54

Query Match      35.6%; Score 22.4; DB 14; Length 504;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 4 AAGTGGCTAGCTGCGATCAATAAAGCCATTGACCATTCACCAATT 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 276 AGCTTCGGGGCGTGGTCCAAATAAACTCATTTCCCTTAACAAATT 229

RESULT 72
US-09-814-353-17042
; Sequence 17042, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17042
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-17042

Query Match      35.6%; Score 22.4; DB 10; Length 571;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 14 CTCGATACATAAAGCCATTGACCATTCACCAATTGGTGTGCACC 61
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 471 CTGAAACACATAAATGATCTCTCACACAAATTTTGTGCATC 518

RESULT 73
US-10-027-632-55098/c
; Sequence 55098, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 315554
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-315554

Query Match      35.6%; Score 22.4; DB 15; Length 586;
Best Local Similarity 72.5%; Pred. No. 1.4e+02;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 12 AGCTCGATACATAAAGCCATTGACCATTCACCAATT 51
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 585 AGCTGCTTTGATATGGGACATTGACCATTCATGACATT 546

RESULT 75
US-10-027-632-202555

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; Sequence 202555, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 202555
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-202555

Query Match      35.6%; Score 22.4; DB 15; Length 611;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 35; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy      7  TGCTAGCTCGATACATAACGCCATTGACCATTCACACATTCGTGCGACCT 62
Db      411  TTCCAGTTCCTCTCCAGATAGACATTGACCTCCAGCTCTTCAGGTGACCT 466

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Search completed: March 11, 2004, 11:20:29
Job time : 52.7306 secs